

IAP13 Rec'd PCT/PTO 12 DEC 2005

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SEQUENCE LISTING

<110> The Scripps Research Institute
The Regents of the University of California
Wu, Eugene
Nemerow, Glen R.
Stewart, Phoebe

<120> MODIFIED FIBER PROTEINS FOR EFFICIENT
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24

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tat gac aca gaa acc ggg cct cca act gtg ccc ttt ctt acc cct cca	96
Tyr Asp Thr Glu Thr Gly Pro Pro Thr Val Pro Phe Leu Thr Pro Pro	
20 25 30	
ttt gtt tca ccc aat ggt ttc caa gaa agt ccc cct gga gtt ctc tct	144
Phe Val Ser Pro Asn Gly Phe Gln Glu Ser Pro Pro Gly Val Leu Ser	
35 40 45	
cta cgc gtc tcc gaa cct ttg gac acc tcc cac ggc atg ctt gcg ctt	192
Ieu Arg Val Ser Glu Pro Leu Asp Thr Ser His Gly Met Leu Ala Leu	
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aaa atg ggc agc ggt ctt acc cta gac aag gcc gga aac ctc acc tcc	240
Lys Met Gly Ser Gly Leu Thr Leu Asp Lys Ala Gly Asn Leu Thr Ser	
65 70 75 80	
caa aat gta acc act gtt act cag cca ctt aaa aaa aca aag tca aac	288
Gln Asn Val Thr Val Thr Gln Pro Leu Lys Lys Thr Lys Ser Asn	
85 90 95	
ata agt ttg gac acc tcc gca cca ctt aca att acc tca ggc gcc cta	336
Ile Ser Leu Asp Thr Ser Ala Pro Leu Thr Ile Thr Ser Gly Ala Leu	
100 105 110	
aca gtg gca acc acc gct cct ctg ata gtt act agc ggc gct ctt agc	384
Thr Val Ala Thr Ala Pro Leu Ile Val Thr Ser Gly Ala Leu Ser	
115 120 125	
gta cag tca caa gcc cca ctg acc gtg caa gac tcc aaa cta agc att	432
Val Gln Ser Gln Ala Pro Leu Thr Val Gln Asp Ser Lys Leu Ser Ile	
130 135 140	
gct act aaa ggg ccc att aca gtg tca gat gga aag cta gcc ctg caa	480
Ala Thr Lys Gly Pro Ile Thr Val Ser Asp Gly Lys Leu Ala Leu Gln	
145 150 155 160	
aca tca gcc ccc ctc tct ggc agt gac agc gac acc ctt act gta act	528
Thr Ser Ala Pro Leu Ser Gly Ser Asp Ser Asp Thr Leu Thr Val Thr	
165 170 175	
gca tca ccc ccg cta act act gcc acg ggt agc ttg ggc att aac atg	576
Ala Ser Pro Pro Leu Thr Thr Ala Thr Gly Ser Leu Gly Ile Asn Met	
180 185 190	
gaa gat cct att tat gta aat aat gga aaa ata gga att aaa ata agc	624
Glu Asp Pro Ile Tyr Val Asn Asn Gly Lys Ile Gly Ile Lys Ile Ser	
195 200 205	
ggt cct ttg caa gta gca caa aac tcc gat aca cta aca gta gtt act	672
Gly Pro Leu Gln Val Ala Gln Asn Ser Asp Thr Leu Thr Val Val Thr	
210 215 220	
gga cca ggt gtc acc gtt gaa caa aac tcc ctt aga acc aaa gtt gca	720
Gly Pro Gly Val Thr Val Glu Gln Asn Ser Leu Arg Thr Lys Val Ala	

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cca ttt gat gct caa aca aaa cta cgt ctt aaa ctg ggg cag gga ccc Pro Phe Asp Ala Gln Thr Lys Leu Arg Leu Lys Leu Gly Gln Gly Pro 275 280 285				864
ctg tat att aat gca tct cat aac ttg gac ata aac tat aac aga ggc Leu Tyr Ile Asn Ala Ser His Asn Leu Asp Ile Asn Tyr Asn Arg Gly 290 295 300				912
cta tac ctt ttt aat gca tca aac aat act aaa aaa ctg gaa gtt agc Leu Tyr Leu Phe Asn Ala Ser Asn Asn Thr Lys Lys Leu Glu Val Ser 305 310 315 320				960
ata aaa aaa tcc agt gga cta aac ttt gat aat act gcc ata gct ata Ile Lys Lys Ser Ser Gly Leu Asn Phe Asp Asn Thr Ala Ile Ala Ile 325 330 335				1008
aat gca gga aag ggt ctg gag ttt gat aca aac aca tct gag tct cca Asn Ala Gly Lys Gly Leu Glu Phe Asp Thr Asn Thr Ser Glu Ser Pro 340 345 350				1056
gat atc aac cca ata aaa act aaa att ggc tct ggc att gat tac aat Asp Ile Asn Pro Ile Lys Thr Lys Ile Gly Ser Gly Ile Asp Tyr Asn 355 360 365				1104
gaa aac ggt gcc atg att act aaa ctt gga gcg ggt tta agc ttt gac Glu Asn Gly Ala Met Ile Thr Lys Leu Gly Ala Gly Leu Ser Phe Asp 370 375 380				1152
aac tca ggg gcc att aca ata gga aac aaa aat gat gac aaa ctt acc Asn Ser Gly Ala Ile Thr Ile Gly Asn Lys Asn Asp Asp Lys Leu Thr 385 390 395 400				1200
ctg tgg aca acc cca gac cca tct cct aac tgc aga att cat tca gat Leu Trp Thr Thr Pro Asp Pro Ser Pro Asn Cys Arg Ile His Ser Asp 405 410 415				1248
aat gac tgc aaa ttt act ttg gtt ctt aca aaa tgt ggg agt caa gta Asn Asp Cys Lys Phe Thr Leu Val Leu Thr Lys Cys Gly Ser Gln Val 420 425 430				1296
cta gct act gta gct gct ttg gct gta tct gga gat ctt tca tcc atg Leu Ala Thr Val Ala Ala Leu Ala Val Ser Gly Asp Leu Ser Ser Met 435 440 445				1344
aca ggc acc gtt gca agt gtt agt ata ttc ctt aga ttt gac caa aac Thr Gly Thr Val Ala Ser Val Ser Ile Phe Leu Arg Phe Asp Gln Asn 450 455 460				1392
ggg gtt cta atg gag aac tcc tca ctt aaa aaa cat tac tgg aac ttt Gly Val Leu Met Glu Asn Ser Ser Leu Lys Lys His Tyr Trp Asn Phe 465 470 475 480				1440

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aga aat ggg aac tca act aat gca aat cca tac aca aat gca gtt gga	1488
Arg Asn Gly Asn Ser Thr Asn Ala Asn Pro Tyr Thr Asn Ala Val Gly	
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ttt atg cct aac ctt cta gcc tat cca aaa acc caa agt caa act gct	1536
Phe Met Pro Asn Leu Leu Ala Tyr Pro Lys Thr Gln Ser Gln Thr Ala	
500 505 510	
aaa aat aac att gtc agt caa gtt tac ttg cat ggt gat aaa act aaa	1584
Lys Asn Asn Ile Val Ser Gln Val Tyr Leu His Gly Asp Lys Thr Lys	
515 520 525	
cct atg ata ctt acc att aca ctt aat ggc act agt gaa tcc aca gaa	1632
Pro Met Ile Leu Thr Ile Thr Leu Asn Gly Thr Ser Glu Ser Thr Glu	
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act agc gag gta agc act tac tct atg tct ttt aca tgg tcc tgg gaa	1680
Thr Ser Glu Val Ser Thr Tyr Ser Met Ser Phe Thr Trp Ser Trp Glu	
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agt gga aaa tac acc act gaa act ttt gct acc aac tct tac acc ttc	1728
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Ser Tyr Ile Ala Gln Glu *	
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 Phe Val Ser Pro Asn Gly Phe Gln Glu Ser Pro Pro Gly Val Leu Ser
 35 40 45
 Leu Arg Val Ser Glu Pro Leu Asp Thr Ser His Gly Met Leu Ala Leu
 50 55 60
 Lys Met Gly Ser Gly Leu Thr Leu Asp Lys Ala Gly Asn Leu Thr Ser
 65 70 75 80
 Gln Asn Val Thr Thr Val Thr Gln Pro Leu Lys Lys Thr Lys Ser Asn
 85 90 95
 Ile Ser Leu Asp Thr Ser Ala Pro Leu Thr Ile Thr Ser Gly Ala Leu
 100 105 110
 Thr Val Ala Thr Thr Ala Pro Leu Ile Val Thr Ser Gly Ala Leu Ser
 115 120 125
 Val Gln Ser Gln Ala Pro Leu Thr Val Gln Asp Ser Lys Leu Ser Ile
 130 135 140
 Ala Thr Lys Gly Pro Ile Thr Val Ser Asp Gly Lys Leu Ala Leu Gln
 145 150 155 160
 Thr Ser Ala Pro Leu Ser Gly Ser Asp Ser Asp Thr Leu Thr Val Thr
 165 170 175
 Ala Ser Pro Pro Leu Thr Thr Ala Thr Gly Ser Leu Gly Ile Asn Met
 180 185 190
 Glu Asp Pro Ile Tyr Val Asn Asn Gly Lys Ile Gly Ile Lys Ile Ser

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Gly Pro Gly Val Thr Val Glu Gln Asn Ser Leu Arg Thr Lys Val Ala		
225	230	235
Gly Ala Ile Gly Tyr Asp Ser Ser Asn Asn Met Glu Ile Lys Thr Gly		240
245	250	255
Gly Gly Met Arg Ile Asn Asn Asn Leu Ile Leu Asp Val Asp Tyr		
260	265	270
Pro Phe Asp Ala Gln Thr Lys Leu Arg Leu Lys Leu Gly Gln Gly Pro		
275	280	285
Leu Tyr Ile Asn Ala Ser His Asn Leu Asp Ile Asn Tyr Asn Arg Gly		
290	295	300
Leu Tyr Leu Phe Asn Ala Ser Asn Asn Thr Lys Lys Leu Glu Val Ser		
305	310	315
Ile Lys Lys Ser Ser Gly Leu Asn Phe Asp Asn Thr Ala Ile Ala Ile		320
325	330	335
Asn Ala Gly Lys Gly Leu Glu Phe Asp Thr Asn Thr Ser Glu Ser Pro		
340	345	350
Asp Ile Asn Pro Ile Lys Thr Lys Ile Gly Ser Gly Ile Asp Tyr Asn		
355	360	365
Glu Asn Gly Ala Met Ile Thr Lys Leu Gly Ala Gly Leu Ser Phe Asp		
370	375	380
Asn Ser Gly Ala Ile Thr Ile Gly Asn Lys Asn Asp Asp Lys Leu Thr		
385	390	395
Leu Trp Thr Thr Pro Asp Pro Ser Pro Asn Cys Arg Ile His Ser Asp		400
405	410	415
Asn Asp Cys Lys Phe Thr Leu Val Leu Thr Lys Cys Gly Ser Gln Val		
420	425	430
Leu Ala Thr Val Ala Ala Leu Ala Val Ser Gly Asp Leu Ser Ser Met		
435	440	445
Thr Gly Thr Val Ala Ser Val Ser Ile Phe Leu Arg Phe Asp Gln Asn		
450	455	460
Gly Val Leu Met Glu Asn Ser Ser Leu Lys Lys His Tyr Trp Asn Phe		
465	470	475
Arg Asn Gly Asn Ser Thr Asn Ala Asn Pro Tyr Thr Asn Ala Val Gly		480
485	490	495
Phe Met Pro Asn Leu Leu Ala Tyr Pro Lys Thr Gln Ser Gln Thr Ala		
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Lys Asn Asn Ile Val Ser Gln Val Tyr Leu His Gly Asp Lys Thr Lys		
515	520	525
Pro Met Ile Leu Thr Ile Thr Leu Asn Gly Thr Ser Glu Ser Thr Glu		
530	535	540
Thr Ser Glu Val Ser Thr Tyr Ser Met Ser Phe Thr Trp Ser Trp Glu		
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Ser Gly Lys Tyr Thr Thr Glu Thr Phe Ala Thr Asn Ser Tyr Thr Phe		560
565	570	575
Ser Tyr Ile Ala Gln Glu		
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<210> 34
 <211> 1746
 <212> DNA
 <213> Adenovirus serotype 5 fiber

<220>
 <221> CDS
 <222> (1)...(1746)
 <400> 34

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atg aag cgc gca aga ccg tct gaa gat acc ttc aac ccc gtg tat cca	48
Met Lys Arg Ala Arg Pro Ser Glu Asp Thr Phe Asn Pro Val Tyr Pro	
1 5 10 15	
tat gac acg gaa acc ggt cct cca act gtg cct ttt ctt act cct ccc	96
Tyr Asp Thr Glu Thr Gly Pro Pro Thr Val Pro Phe Leu Thr Pro Pro	
20 25 30	
ttt gta tcc ccc aat ggg ttt caa gag agt ccc cct ggg gta ctc tct	144
Phe Val Ser Pro Asn Gly Phe Gln Glu Ser Pro Pro Gly Val Leu Ser	
35 40 45	
ttg cgc cta tcc gaa cct cta gtt acc tcc aat ggc atg ctt gcg ctc	192
Leu Arg Leu Ser Glu Pro Leu Val Thr Ser Asn Gly Met Leu Ala Leu	
50 55 60	
aaa atg ggc aac ggc ctc tct ctg gac gag gcc ggc aac ctt acc tcc	240
Lys Met Gly Asn Gly Leu Ser Leu Asp Glu Ala Gly Asn Leu Thr Ser	
65 70 75 80	
caa aat gta acc act gtg agc cca cct ctc aaa aaa acc aag tca aac	288
Gln Asn Val Thr Thr Val Ser Pro Pro Leu Lys Lys Thr Lys Ser Asn	
85 90 95	
ata aac ctg gaa ata tct gca ccc ctc aca gtt acc tca gaa gcc cta	336
Ile Asn Leu Glu Ile Ser Ala Pro Leu Thr Val Thr Ser Glu Ala Leu	
100 105 110	
act gtg gct gcc gcc gca cct cta atg gtc gcg ggc aac aca ctc acc	384
Thr Val Ala Ala Ala Pro Leu Met Val Ala Gly Asn Thr Leu Thr	
115 120 125	
atg caa tca cag gcc ccg cta acc gtg cac gac tcc aaa ctt agc att	432
Met Gln Ser Gln Ala Pro Leu Thr Val His Asp Ser Lys Leu Ser Ile	
130 135 140	
gcc acc caa gga ccc ctc aca gtg tca gaa gga aag cta gcc ctg caa	480
Ala Thr Gln Gly Pro Leu Thr Val Ser Glu Gly Lys Leu Ala Leu Gln	
145 150 155 160	
aca tca ggc ccc ctc acc acc acc gat agc agt acc ctt act atc act	528
Thr Ser Gly Pro Leu Thr Thr Asp Ser Ser Thr Leu Thr Ile Thr	
165 170 175	
gcc tca ccc cct cta act act gcc act ggt agc ttg ggc att gac ttg	576
Ala Ser Pro Pro Leu Thr Thr Ala Thr Gly Ser Leu Gly Ile Asp Leu	
180 185 190	
aaa gag ccc att tat aca caa aat gga aaa cta gga cta aag tac ggg	624
Lys Glu Pro Ile Tyr Thr Gln Asn Gly Lys Leu Gly Leu Lys Tyr Gly	
195 200 205	
gct cct ttg cat gta aca gac gac cta aac act ttg acc gta gca act	672
Ala Pro Leu His Val Thr Asp Asp Leu Asn Thr Leu Thr Val Ala Thr	
210 215 220	
ggt cca ggt gtg act att aat aat act tcc ttg caa act aaa gtt act	720
Gly Pro Gly Val Thr Ile Asn Asn Thr Ser Leu Gln Thr Lys Val Thr	
225 230 235 240	
gga gcc ttg ggt ttt gat tca caa ggc aat atg caa ctt aat gta gca	768

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Gly Ala Leu Gly Phe Asp Ser Gln Gly Asn Met Gln Leu Asn Val Ala			
245	250	255	
gga gga cta agg att gat tct caa aac aga cgc ctt ata ctt gat gtt		816	
Gly Gly Leu Arg Ile Asp Ser Gln Asn Arg Arg Leu Ile Leu Asp Val			
260	265	270	
agt tat ccg ttt gat gct caa aac caa cta aat cta aga cta gga cag		864	
Ser Tyr Pro Phe Asp Ala Gln Asn Gln Leu Asn Leu Arg Leu Gly Gln			
275	280	285	
ggc cct ctt ttt ata aac tca gcc cac aac ttg gat att aac tac aac		912	
Gly Pro Leu Phe Ile Asn Ser Ala His Asn Leu Asp Ile Asn Tyr Asn			
290	295	300	
aaa ggc ctt tac ttg ttt aca gct tca aac aat tcc aaa aag ctt gag		960	
Lys Gly Leu Tyr Leu Phe Thr Ala Ser Asn Asn Ser Lys Lys Leu Glu			
305	310	315	320
gtt aac cta agc act gcc aag ggg ttg atg ttt gac gct aca gcc ata		1008	
Val Asn Leu Ser Thr Ala Lys Gly Leu Met Phe Asp Ala Thr Ala Ile			
325	330	335	
gcc att aat gca gga gat ggg ctt gaa ttt ggt tca cct aat gca cca		1056	
Ala Ile Asn Ala Gly Asp Gly Leu Glu Phe Gly Ser Pro Asn Ala Pro			
340	345	350	
aac aca aat ccc ctc aaa aca aaa att ggc cat ggc cta gaa ttt gat		1104	
Asn Thr Asn Pro Leu Lys Thr Ile Gly His Gly Leu Glu Phe Asp			
355	360	365	
tca aac aag gct atg gtt cct aaa cta gga act ggc ctt agt ttt gac		1152	
Ser Asn Lys Ala Met Val Pro Lys Leu Gly Thr Gly Leu Ser Phe Asp			
370	375	380	
agc aca ggt gcc att aca gta gga aac aaa aat aat gat aag cta act		1200	
Ser Thr Gly Ala Ile Thr Val Gly Asn Lys Asn Asn Asp Lys Leu Thr			
385	390	395	400
ttg tgg acc aca cca gct cca tct cct aac tgt aga cta aat gca gag		1248	
Leu Trp Thr Thr Pro Ala Pro Ser Pro Asn Cys Arg Leu Asn Ala Glu			
405	410	415	
aaa gat gct aaa ctc act ttg gtc tta aca aaa tgt ggc agt caa ata		1296	
Lys Asp Ala Lys Leu Thr Leu Val Leu Thr Lys Cys Gly Ser Gln Ile			
420	425	430	
ctt gct aca gtt tca gtt ttg gct gtt aaa ggc agt ttg gct cca ata		1344	
Leu Ala Thr Val Ser Val Leu Ala Val Lys Gly Ser Leu Ala Pro Ile			
435	440	445	
tct gga aca gtt caa agt gct cat ctt att ata aga ttt gac gaa aat		1392	
Ser Gly Thr Val Gln Ser Ala His Leu Ile Ile Arg Phe Asp Glu Asn			
450	455	460	
gga gtg cta cta aac aat tcc ttc ctg gac cca gaa tat tgg aac ttt		1440	
Gly Val Leu Leu Asn Asn Ser Phe Leu Asp Pro Glu Tyr Trp Asn Phe			
465	470	475	480
aga aat gga gat ctt act gaa ggc aca gcc tat aca aac gct gtt gga		1488	
Arg Asn Gly Asp Leu Thr Glu Gly Thr Ala Tyr Thr Asn Ala Val Gly			

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485

490

495

ttt atg cct aac cta tca gct tat cca aaa tct cac ggt aaa act gcc 1536
 Phe Met Pro Asn Leu Ser Ala Tyr Pro Lys Ser His Gly Lys Thr Ala
 500 505 510

aaa agt aac att gtc agt caa gtt tac tta aac gga gac aaa act aaa 1584
 Lys Ser Asn Ile Val Ser Gln Val Tyr Leu Asn Gly Asp Lys Thr Lys
 515 520 525

cct gta aca cta acc att aca cta aac ggt aca cag gaa aca gga gac 1632
 Pro Val Thr Leu Thr Ile Thr Leu Asn Gly Thr Gln Glu Thr Gly Asp
 530 535 540

aca act cca agt gca tac tct atg tca ttt tca tgg gac tgg tct ggc 1680
 Thr Thr Pro Ser Ala Tyr Ser Met Ser Phe Ser Trp Asp Trp Ser Gly
 545 550 555 560

cac aac tac att aat gaa ata ttt gcc aca tcc tct tac act ttt tca 1728
 His Asn Tyr Ile Asn Glu Ile Phe Ala Thr Ser Ser Tyr Thr Phe Ser
 565 570 575

tac att gcc caa gaa taa 1746
 Tyr Ile Ala Gln Glu *
 580

<210> 35

<211> 581

<212> PRT

<213> Adenovirus serotype 5 fiber

<400> 35

Met Lys Arg Ala Arg Pro Ser Glu Asp Thr Phe Asn Pro Val Tyr Pro
 1 5 10 15
 Tyr Asp Thr Glu Thr Gly Pro Pro Thr Val Pro Phe Leu Thr Pro Pro
 20 25 30
 Phe Val Ser Pro Asn Gly Phe Gln Glu Ser Pro Pro Gly Val Leu Ser
 35 40 45
 Leu Arg Leu Ser Glu Pro Leu Val Thr Ser Asn Gly Met Leu Ala Leu
 50 55 60
 Lys Met Gly Asn Gly Leu Ser Leu Asp Glu Ala Gly Asn Leu Thr Ser
 65 70 75 80
 Gln Asn Val Thr Thr Val Ser Pro Pro Leu Lys Lys Thr Lys Ser Asn
 85 90 95
 Ile Asn Leu Glu Ile Ser Ala Pro Leu Thr Val Thr Ser Glu Ala Leu
 100 105 110
 Thr Val Ala Ala Ala Pro Leu Met Val Ala Gly Asn Thr Leu Thr
 115 120 125
 Met Gln Ser Gln Ala Pro Leu Thr Val His Asp Ser Lys Leu Ser Ile
 130 135 140
 Ala Thr Gln Gly Pro Leu Thr Val Ser Glu Gly Lys Leu Ala Leu Gln
 145 150 155 160
 Thr Ser Gly Pro Leu Thr Thr Asp Ser Ser Thr Leu Thr Ile Thr
 165 170 175
 Ala Ser Pro Pro Leu Thr Thr Ala Thr Gly Ser Leu Gly Ile Asp Leu
 180 185 190
 Lys Glu Pro Ile Tyr Thr Gln Asn Gly Lys Leu Gly Leu Lys Tyr Gly
 195 200 205
 Ala Pro Leu His Val Thr Asp Asp Leu Asn Thr Leu Thr Val Ala Thr
 210 215 220

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Gly Pro Gly Val Thr Ile Asn Asn Thr Ser Leu Gln Thr Lys Val Thr
 225 230 235 240
 Gly Ala Leu Gly Phe Asp Ser Gln Gly Asn Met Gln Leu Asn Val Ala
 245 250 255
 Gly Gly Leu Arg Ile Asp Ser Gln Asn Arg Arg Leu Ile Leu Asp Val
 260 265 270
 Ser Tyr Pro Phe Asp Ala Gln Asn Gln Leu Asn Leu Arg Leu Gly Gln
 275 280 285
 Gly Pro Leu Phe Ile Asn Ser Ala His Asn Leu Asp Ile Asn Tyr Asn
 290 295 300
 Lys Gly Leu Tyr Leu Phe Thr Ala Ser Asn Asn Ser Lys Lys Leu Glu
 305 310 315 320
 Val Asn Leu Ser Thr Ala Lys Gly Leu Met Phe Asp Ala Thr Ala Ile
 325 330 335
 Ala Ile Asn Ala Gly Asp Gly Leu Glu Phe Gly Ser Pro Asn Ala Pro
 340 345 350
 Asn Thr Asn Pro Leu Lys Thr Lys Ile Gly His Gly Leu Glu Phe Asp
 355 360 365
 Ser Asn Lys Ala Met Val Pro Lys Leu Gly Thr Gly Leu Ser Phe Asp
 370 375 380
 Ser Thr Gly Ala Ile Thr Val Gly Asn Lys Asn Asn Asp Lys Leu Thr
 385 390 395 400
 Leu Trp Thr Thr Pro Ala Pro Ser Pro Asn Cys Arg Leu Asn Ala Glu
 405 410 415
 Lys Asp Ala Lys Leu Thr Leu Val Leu Thr Lys Cys Gly Ser Gln Ile
 420 425 430
 Leu Ala Thr Val Ser Val Leu Ala Val Lys Gly Ser Leu Ala Pro Ile
 435 440 445
 Ser Gly Thr Val Gln Ser Ala His Leu Ile Ile Arg Phe Asp Glu Asn
 450 455 460
 Gly Val Leu Leu Asn Asn Ser Phe Leu Asp Pro Glu Tyr Trp Asn Phe
 465 470 475 480
 Arg Asn Gly Asp Leu Thr Glu Gly Thr Ala Tyr Thr Asn Ala Val Gly
 485 490 495
 Phe Met Pro Asn Leu Ser Ala Tyr Pro Lys Ser His Gly Lys Thr Ala
 500 505 510
 Lys Ser Asn Ile Val Ser Gln Val Tyr Leu Asn Gly Asp Lys Thr Lys
 515 520 525
 Pro Val Thr Leu Thr Ile Thr Leu Asn Gly Thr Gln Glu Thr Gly Asp
 530 535 540
 Thr Thr Pro Ser Ala Tyr Ser Met Ser Phe Ser Trp Asp Trp Ser Gly
 545 550 555 560
 His Asn Tyr Ile Asn Glu Ile Phe Ala Thr Ser Ser Tyr Thr Phe Ser
 565 570 575
 Tyr Ile Ala Gln Glu
 580

<210> 36
 <211> 1098
 <212> DNA
 <213> Adenovirus serotype 37 fiber

<220>
 <221> CDS
 <222> (1)...(1098)

<400> 36
 atg tca aag agg ctc cgg gtg gaa gat gac ttc aac ccc gtc tac ccc 48
 Met Ser Lys Arg Leu Arg Val Glu Asp Asp Phe Asn Pro Val Tyr Pro
 1 5 10 15

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tat ggc tac gcg cgg aat cag aat atc ccc ttc ctc act ccc ccc ttt	96
Tyr Gly Tyr Ala Arg Asn Gln Asn Ile Pro Phe Leu Thr Pro Pro Phe	
20 25 30	
gtc tcc tcc gat gga ttc aaa aac ttc ccc cct ggg gta ctg tca ctc	144
Val Ser Ser Asp Gly Phe Lys Asn Phe Pro Pro Gly Val Leu Ser Leu	
35 40 45	
aaa ctg gct gat cca atc acc att acc aat ggg gat gta tcc ctc aag	192
Lys Leu Ala Asp Pro Ile Thr Ile Thr Asn Gly Asp Val Ser Leu Lys	
50 55 60	
gtg gga ggt ggt ctc act ttg caa gat gga agc cta act gta aac cct	240
Val Gly Gly Leu Thr Leu Gln Asp Gly Ser Leu Thr Val Asn Pro	
65 70 75 80	
aag gct cca ctg caa gtt aat act gat aaa aaa ctt gag ctt gca tat	288
Lys Ala Pro Leu Gln Val Asn Thr Asp Lys Lys Leu Glu Leu Ala Tyr	
85 90 95	
gat aat cca ttt gaa agt agt gct aat aaa ctt agt tta aaa gta gga	336
Asp Asn Pro Phe Glu Ser Ser Ala Asn Lys Leu Ser Leu Lys Val Gly	
100 105 110	
cat gga tta aaa gta tta gat gaa aaa agt gct gcg ggg tta aaa gat	384
His Gly Leu Lys Val Leu Asp Glu Lys Ser Ala Ala Gly Leu Lys Asp	
115 120 125	
tta att ggc aaa ctt gtg gtt tta aca gga aaa gga ata ggc act gaa	432
Leu Ile Gly Lys Leu Val Val Leu Thr Gly Lys Gly Ile Gly Thr Glu	
130 135 140	
aat tta gaa aat aca gat ggt agc agc aga gga att ggt ata aat gta	480
Asn Leu Glu Asn Thr Asp Gly Ser Ser Arg Gly Ile Gly Ile Asn Val	
145 150 155 160	
aga gca aga gaa ggg ttg aca ttt gac aat gat gga tac ttg gta gca	528
Arg Ala Arg Glu Gly Leu Thr Phe Asp Asn Asp Gly Tyr Leu Val Ala	
165 170 175	
tgg aac cca aag tat gac acg cgc aca ctt tgg aca aca cca gac aca	576
Trp Asn Pro Lys Tyr Asp Thr Arg Thr Leu Trp Thr Thr Pro Asp Thr	
180 185 190	
tct cca aac tgc aca att gct caa gat aag gac tct aaa ctc act ttg	624
Ser Pro Asn Cys Thr Ile Ala Gln Asp Lys Asp Ser Lys Leu Thr Leu	
195 200 205	
gta ctt aca aag tgt gga agt caa ata tta gct aat gtg tct ttg att	672
Val Leu Thr Lys Cys Gly Ser Gln Ile Leu Ala Asn Val Ser Leu Ile	
210 215 220	
gtg gtc gca gga aag tac cac atc ata aat aat aag aca aat cca aaa	720
Val Val Ala Gly Lys Tyr His Ile Ile Asn Lys Thr Asn Pro Lys	
225 230 235 240	
ata aaa agt ttt act att aaa ctg cta ttt aat aag aac gga gtg ctt	768
Ile Lys Ser Phe Thr Ile Lys Leu Leu Phe Asn Lys Asn Gly Val Leu	
245 250 255	

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tta gac aac tca aat ctt gga aaa gct tat tgg aac ttt aga agt gga	816
Leu Asp Asn Ser Asn Leu Gly Lys Ala Tyr Trp Asn Phe Arg Ser Gly	
260 265 270	
aat tcc aat gtt tcg aca gct tat gaa aaa gca att ggt ttt atg cct	864
Asn Ser Asn Val Ser Thr Ala Tyr Glu Lys Ala Ile Gly Phe Met Pro	
275 280 285	
aat ttg gta gcg tat cca aaa ccc agt aat tct aaa aaa tat gca aga	912
Asn Leu Val Ala Tyr Pro Lys Pro Ser Asn Ser Lys Lys Tyr Ala Arg	
290 295 300	
gac ata gtt tat gga act ata tat ctt ggt gga aaa cct gat cag cca	960
Asp Ile Val Tyr Gly Thr Ile Tyr Leu Gly Gly Lys Pro Asp Gln Pro	
305 310 315 320	
gca gtc att aaa act acc ttt aac caa gaa act gga tgt gaa tac tct	1008
Ala Val Ile Lys Thr Phe Asn Gln Glu Thr Gly Cys Glu Tyr Ser	
325 330 335	
atc aca ttt aac ttt agt tgg tcc aaa acc tat gaa aat gtt gaa ttt	1056
Ile Thr Phe Asn Phe Ser Trp Ser Lys Thr Tyr Glu Asn Val Glu Phe	
340 345 350	
gaa acc acc tct ttt acc ttc tcc tat att gcc caa gaa tga	1098
Glu Thr Thr Ser Phe Thr Phe Ser Tyr Ile Ala Gln Glu *	
355 360 365	

<210> 37

<211> 365

<212> PRT

<213> Adenovirus serotype 37 fiber

<400> 37

Met Ser Lys Arg Leu Arg Val Glu Asp Asp Phe Asn Pro Val Tyr Pro	
1 5 10 15	
Tyr Gly Tyr Ala Arg Asn Gln Asn Ile Pro Phe Leu Thr Pro Pro Phe	
20 25 30	
Val Ser Ser Asp Gly Phe Lys Asn Phe Pro Pro Gly Val Leu Ser Leu	
35 40 45	
Lys Leu Ala Asp Pro Ile Thr Ile Thr Asn Gly Asp Val Ser Leu Lys	
50 55 60	
Val Gly Gly Leu Thr Leu Gln Asp Gly Ser Leu Thr Val Asn Pro	
65 70 75 80	
Lys Ala Pro Leu Gln Val Asn Thr Asp Lys Lys Leu Glu Leu Ala Tyr	
85 90 95	
Asp Asn Pro Phe Glu Ser Ser Ala Asn Lys Leu Ser Leu Lys Val Gly	
100 105 110	
His Gly Leu Lys Val Leu Asp Glu Lys Ser Ala Ala Gly Leu Lys Asp	
115 120 125	
Leu Ile Gly Lys Leu Val Val Leu Thr Gly Lys Gly Ile Gly Thr Glu	
130 135 140	
Asn Leu Glu Asn Thr Asp Gly Ser Ser Arg Gly Ile Gly Ile Asn Val	
145 150 155 160	
Arg Ala Arg Glu Gly Leu Thr Phe Asp Asn Asp Gly Tyr Leu Val Ala	
165 170 175	
Trp Asn Pro Lys Tyr Asp Thr Arg Thr Leu Trp Thr Pro Asp Thr	
180 185 190	
Ser Pro Asn Cys Thr Ile Ala Gln Asp Lys Asp Ser Lys Leu Thr Leu	

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195	200	205
Val Leu Thr Lys Cys Gly Ser Gln Ile Leu Ala Asn Val Ser Leu Ile		
210	215	220
Val Val Ala Gly Lys Tyr His Ile Ile Asn Asn Lys Thr Asn Pro Lys		
225	230	235
Ile Lys Ser Phe Thr Ile Lys Leu Leu Phe Asn Lys Asn Gly Val Leu		
245	250	255
Leu Asp Asn Ser Asn Leu Gly Lys Ala Tyr Trp Asn Phe Arg Ser Gly		
260	265	270
Asn Ser Asn Val Ser Thr Ala Tyr Glu Lys Ala Ile Gly Phe Met Pro		
275	280	285
Asn Leu Val Ala Tyr Pro Lys Pro Ser Asn Ser Lys Lys Tyr Ala Arg		
290	295	300
Asp Ile Val Tyr Gly Thr Ile Tyr Leu Gly Gly Lys Pro Asp Gln Pro		
305	310	315
Ala Val Ile Lys Thr Thr Phe Asn Gln Glu Thr Gly Cys Glu Tyr Ser		
325	330	335
Ile Thr Phe Asn Phe Ser Trp Ser Lys Thr Tyr Glu Asn Val Glu Phe		
340	345	350
Glu Thr Thr Ser Phe Thr Phe Ser Tyr Ile Ala Gln Glu		
355	360	365

<210> 38

<211> 1098

<212> DNA

<213> Adenovirus serotype 19p fiber

<220>

<221> CDS

<222> (1)...(1098)

<400> 38

atg tca aag agg ctc cgg gtg gaa gat gac ttc aac ccc gtc tac ccc	48
Met Ser Lys Arg Leu Arg Val Glu Asp Asp Phe Asn Pro Val Tyr Pro	
1 5 10 15	

tat ggc tac gcg cgg aat cag aat atc ccc ttc ctc act ccc ccc ttt	96
Tyr Gly Tyr Ala Arg Asn Gln Asn Ile Pro Phe Leu Thr Pro Pro Phe	
20 25 30	

gtc tcc tcc gat gga ttc aaa aac ttc ccc cct ggg gta ctg tca ctc	144
Val Ser Ser Asp Gly Phe Lys Asn Phe Pro Pro Gly Val Leu Ser Leu	
35 40 45	

aaa ctg gct gat cca atc acc att acc aat ggg gat gta tcc ctc aag	192
Lys Leu Ala Asp Pro Ile Thr Ile Thr Asn Gly Asp Val Ser Leu Lys	
50 55 60	

gtg gga ggt ggt ctc act ttg caa gat gga agc cta act gta aac cct	240
Val Gly Gly Leu Thr Leu Gln Asp Gly Ser Leu Thr Val Asn Pro	
65 70 75 80	

aag gct cca ctg caa gtt act act gat aaa aaa ctt gag ctt gca tat	288
Lys Ala Pro Leu Gln Val Thr Asp Lys Lys Leu Glu Leu Ala Tyr	
85 90 95	

gat aat cca ttt gaa tgt agt gct aat aaa ttt agt tta aaa gta gga	336
Asp Asn Pro Phe Glu Cys Ser Ala Asn Lys Phe Ser Leu Lys Val Gly	
100 105 110	

-26-

cat gga tta aaa gta tta gat gaa aaa agt gct gcg ggg tta aaa gat	384
His Gly Leu Lys Val Leu Asp Glu Lys Ser Ala Ala Gly Leu Lys Asp	
115 120 125	
tta att ggc aaa ctt gtg gtt tta aca gga aaa gga ata ggc act gaa	432
Leu Ile Gly Lys Leu Val Val Leu Thr Gly Lys Gly Ile Gly Thr Glu	
130 135 140	
aat tta gaa aat aca gat ggt agc agc aga gga att ggt ata aat gta	480
Asn Leu Glu Asn Thr Asp Gly Ser Ser Arg Gly Ile Gly Ile Asn Val	
145 150 155 160	
aga gca aga gaa ggg ttg aca ttt gac aat gat gga tac ttg gta gca	528
Arg Ala Arg Glu Gly Leu Thr Phe Asp Asn Asp Gly Tyr Leu Val Ala	
165 170 175	
tgg aac cca aag tat gac acg cgc aca ctt tgg aca aca cca gac aca	576
Trp Asn Pro Lys Tyr Asp Thr Arg Thr Leu Trp Thr Pro Asp Thr	
180 185 190	
tct cca aac tgc aca att gct cag gat aag gac tct aaa ctc act ttg	624
Ser Pro Asn Cys Thr Ile Ala Gln Asp Lys Asp Ser Lys Leu Thr Leu	
195 200 205	
gta ctt aca aag tgt gga agt caa ata tta gct aat gtg tct ttg att	672
Val Leu Thr Lys Cys Gly Ser Gln Ile Leu Ala Asn Val Ser Leu Ile	
210 215 220	
gtg gtc gca gga aag tac cac atc ata aat aat aag aca aat cca gaa	720
Val Val Ala Gly Lys Tyr His Ile Ile Asn Asn Lys Thr Asn Pro Glu	
225 230 235 240	
ata aaa agt ttt act att aaa ctg tta ttt aat aag aac gga gtg ctt	768
Ile Lys Ser Phe Thr Ile Lys Leu Leu Phe Asn Lys Asn Gly Val Leu	
245 250 255	
tta gac aac tca aat ctt gga aaa gct tat tgg aac ttt aga agt gga	816
Leu Asp Asn Ser Asn Leu Gly Lys Ala Tyr Trp Asn Phe Arg Ser Gly	
260 265 270	
aat tcc aat gtt tcg aca gct tat gaa aaa gca att ggt ttt atg cct	864
Asn Ser Asn Val Ser Thr Ala Tyr Glu Lys Ala Ile Gly Phe Met Pro	
275 280 285	
aat tta gta gcg tat cca aaa ccc agt aat tct aaa aaa tat gca aga	912
Asn Leu Val Ala Tyr Pro Lys Pro Ser Asn Ser Lys Lys Tyr Ala Arg	
290 295 300	
gac ata gtt tat gga act ata tat ctt ggt gga aaa cct gat cag cca	960
Asp Ile Val Tyr Gly Thr Ile Tyr Leu Gly Gly Lys Pro Asp Gln Pro	
305 310 315 320	
gca gtc att aaa act acc ttt aac caa gaa act gga tgt gaa tac tct	1008
Ala Val Ile Lys Thr Thr Phe Asn Gln Glu Thr Gly Cys Glu Tyr Ser	
325 330 335	
atc aca ttt gac ttt agt tgg tcc aaa acc tat gaa aat gtt gaa ttt	1056
Ile Thr Phe Asp Phe Ser Trp Ser Lys Thr Tyr Glu Asn Val Glu Phe	
340 345 350	
gaa acc acc tct ttt acc ttc tcc tat att gcc caa gaa tga	1098

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Glu Thr Thr Ser Phe Thr Phe Ser Tyr Ile Ala Gln Glu *
 355 360 365

<210> 39
 <211> 365
 <212> PRT
 <213> Adenovirus serotype 19p fiber

<400> 39
 Met Ser Lys Arg Leu Arg Val Glu Asp Asp Phe Asn Pro Val Tyr Pro
 1 5 10 15
 Tyr Gly Tyr Ala Arg Asn Gln Asn Ile Pro Phe Leu Thr Pro Pro Phe
 20 25 30
 Val Ser Ser Asp Gly Phe Lys Asn Phe Pro Pro Gly Val Leu Ser Leu
 35 40 45
 Lys Leu Ala Asp Pro Ile Thr Ile Thr Asn Gly Asp Val Ser Leu Lys
 50 55 60
 Val Gly Gly Gly Leu Thr Leu Gln Asp Gly Ser Leu Thr Val Asn Pro
 65 70 75 80
 Lys Ala Pro Leu Gln Val Thr Thr Asp Lys Lys Leu Glu Leu Ala Tyr
 85 90 95
 Asp Asn Pro Phe Glu Cys Ser Ala Asn Lys Phe Ser Leu Lys Val Gly
 100 105 110
 His Gly Leu Lys Val Leu Asp Glu Lys Ser Ala Ala Gly Leu Lys Asp
 115 120 125
 Leu Ile Gly Lys Leu Val Val Leu Thr Gly Lys Gly Ile Gly Thr Glu
 130 135 140
 Asn Leu Glu Asn Thr Asp Gly Ser Ser Arg Gly Ile Gly Ile Asn Val
 145 150 155 160
 Arg Ala Arg Glu Gly Leu Thr Phe Asp Asn Asp Gly Tyr Leu Val Ala
 165 170 175
 Trp Asn Pro Lys Tyr Asp Thr Arg Thr Leu Trp Thr Thr Pro Asp Thr
 180 185 190
 Ser Pro Asn Cys Thr Ile Ala Gln Asp Lys Asp Ser Lys Leu Thr Leu
 195 200 205
 Val Leu Thr Lys Cys Gly Ser Gln Ile Leu Ala Asn Val Ser Leu Ile
 210 215 220
 Val Val Ala Gly Lys Tyr His Ile Ile Asn Asn Lys Thr Asn Pro Glu
 225 230 235 240
 Ile Lys Ser Phe Thr Ile Lys Leu Leu Phe Asn Lys Asn Gly Val Leu
 245 250 255
 Leu Asp Asn Ser Asn Leu Gly Lys Ala Tyr Trp Asn Phe Arg Ser Gly
 260 265 270
 Asn Ser Asn Val Ser Thr Ala Tyr Glu Lys Ala Ile Gly Phe Met Pro
 275 280 285
 Asn Leu Val Ala Tyr Pro Lys Pro Ser Asn Ser Lys Lys Tyr Ala Arg
 290 295 300
 Asp Ile Val Tyr Gly Thr Ile Tyr Leu Gly Gly Lys Pro Asp Gln Pro
 305 310 315 320
 Ala Val Ile Lys Thr Thr Phe Asn Gln Glu Thr Gly Cys Glu Tyr Ser
 325 330 335
 Ile Thr Phe Asp Phe Ser Trp Ser Lys Thr Tyr Glu Asn Val Glu Phe
 340 345 350
 Glu Thr Thr Ser Phe Thr Phe Ser Tyr Ile Ala Gln Glu
 355 360 365

<210> 40
 <211> 1228

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<212> DNA
 <213> Adenovirus serotype 9 fiber
 <220>
 <221> CDS
 <222> (50) ... (1138)

<400> 40
 aaggatgtc aaattcctgg tccacaattt tcattgtctt ccctctcag atg tca aag 58
 Met Ser Lys
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agg ctc cgg gtg gaa gat gac ttc aac ccc gtc tac ccc tat ggc tac	106
Arg Leu Arg Val Glu Asp Asp Phe Asn Pro Val Tyr Pro Tyr Gly Tyr	
5 10 15	
gcg cgg aat cag aat atc ccc ttc ctc act ccc ccc ttt gtc tcc tcc	154
Ala Arg Asn Gln Asn Ile Pro Phe Leu Thr Pro Pro Phe Val Ser Ser	
20 25 30 35	
gat gga ttc caa aac ttc ccc cct ggg gtc ctg tca ctc aaa cta gct	202
Asp Gly Phe Gln Asn Phe Pro Pro Gly Val Leu Ser Leu Lys Leu Ala	
40 45 50	
gac cca ata gcc atc gtc aat ggg aat gtc tca ctc aaa gtc gga ggg	250
Asp Pro Ile Ala Ile Val Asn Gly Asn Val Ser Leu Lys Val Gly Gly	
55 60 65	
ggt ctc act ttg caa gat gga act gga aaa cta aca gtc aat gct gat	298
Gly Leu Thr Leu Gln Asp Gly Thr Gly Lys Leu Thr Val Asn Ala Asp	
70 75 80	
cca cct ttg caa ctt aca aac aac aaa tta ggg att gct ttg gac gct	346
Pro Pro Leu Gln Leu Thr Asn Asn Lys Leu Gly Ile Ala Leu Asp Ala	
85 90 95	
cca ttt gat gtt ata gat aat aaa ctc aca ttg tta gcg ggc cat ggc	394
Pro Phe Asp Val Ile Asp Asn Lys Leu Thr Leu Leu Ala Gly His Gly	
100 105 110 115	
ttg tct att ata aca aaa gaa aca tca aca ctg cct ggc ttg agg aat	442
Leu Ser Ile Ile Thr Lys Glu Thr Ser Thr Leu Pro Gly Leu Arg Asn	
120 125 130	
act ctt gta gta tta act gga aag ggt att gga aca gaa tca aca gat	490
Thr Leu Val Val Leu Thr Gly Lys Gly Ile Gly Thr Glu Ser Thr Asp	
135 140 145	
aat ggc gga acg gta tgt gtt aga gtt gga gaa ggt ggc ggc tta tca	538
Asn Gly Thr Val Cys Val Arg Val Gly Glu Gly Gly Leu Ser	
150 155 160	
ttt aat aat gat gga gac ttg gta gca ttt aat aaa aaa gaa gat aag	586
Phe Asn Asn Asp Gly Asp Leu Val Ala Phe Asn Lys Lys Glu Asp Lys	
165 170 175	
cgc acc cta tgg aca act cca gac aca tct cca aat tgc aag att gat	634
Arg Thr Leu Trp Thr Pro Asp Thr Ser Pro Asn Cys Lys Ile Asp	
180 185 190 195	
cag gat aag gac tct aag tta act ctg gtc ctt aca aag tgt gga agt	682

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Gln	Asp	Lys	Asp	Ser	Lys	Leu	Thr	Leu	Val	Leu	Thr	Lys	Cys	Gly	Ser	
200																210
caa	ata	ttg	gct	aat	gtg	tca	tta	att	gtc	gta	gat	ggt	aag	tac	aaa	730
Gln	Ile	Leu	Ala	Asn	Val	Ser	Leu	Ile	Val	Val	Asp	Gly	Lys	Tyr	Lys	
215															225	
att	atc	aat	aac	aat	act	caa	cca	gct	ctc	aaa	gga	ttt	acc	att	aaa	778
Ile	Ile	Asn	Asn	Asn	Thr	Gln	Pro	Ala	Leu	Lys	Gly	Phe	Thr	Ile	Lys	
230															240	
tta	ttg	ttt	gat	gaa	aat	gga	gta	ctt	atg	gaa	tct	tca	aat	ctt	ggt	826
Leu	Leu	Phe	Asp	Glu	Asn	Gly	Val	Leu	Met	Glu	Ser	Ser	Asn	Leu	Gly	
245															255	
aaa	tca	tat	tgg	aac	ttt	aga	aat	gaa	aat	tca	att	atg	tca	aca	gct	874
Lys	Ser	Tyr	Trp	Asn	Phe	Arg	Asn	Glu	Asn	Ser	Ile	Met	Ser	Thr	Ala	
260															275	
tat	gaa	aaa	gct	att	gga	ttc	atg	cct	aat	ttg	gta	gcc	tat	cca	aaa	922
Tyr	Glu	Lys	Ala	Ile	Gly	Phe	Met	Pro	Asn	Leu	Val	Ala	Tyr	Pro	Lys	
280															290	
cct	acc	gct	ggc	tct	aaa	aaa	tat	gca	aga	gat	ata	gtt	tat	gga	aac	970
Pro	Thr	Ala	Gly	Ser	Lys	Tyr	Ala	Arg	Asp	Ile	Val	Tyr	Gly	Asn		
295															305	
atc	tac	ctt	ggg	aag	cca	gat	caa	cca	gta	acc	att	aaa	act	acc		1018
Ile	Tyr	Leu	Gly	Gly	Lys	Pro	Asp	Gln	Pro	Val	Thr	Ile	Lys	Thr	Thr	
310															320	
ttt	aat	cag	gaa	act	gga	tgt	gaa	tat	tct	atc	aca	ttt	gat	ttt	agt	1066
Phe	Asn	Gln	Glu	Thr	Gly	Cys	Glu	Tyr	Ser	Ile	Thr	Phe	Asp	Phe	Ser	
325															335	
tgg	gcc	aag	act	tat	gta	aat	gtt	gaa	ttt	gaa	aca	acc	tct	ttt	acc	1114
Trp	Ala	Lys	Thr	Tyr	Val	Asn	Val	Glu	Phe	Glu	Thr	Thr	Ser	Phe	Thr	
340															355	
ttt	tcc	tat	atc	gcc	caa	gaa	tga	aagaccaata	aacgttttt	tcatttcaaa						1168
Phe	Ser	Tyr	Ile	Ala	Gln	Glu	*									
360																
attttcatgt atctttattt atttttacac cagcacgggt agtcagtctc ccaccaccag																1228

<210> 41
 <211> 362
 <212> PRT
 <213> Adenovirus serotype 9 fiber

<400> 41
 Met Ser Lys Arg Leu Arg Val Glu Asp Asp Phe Asn Pro Val Tyr Pro
 1 5 10 15
 Tyr Gly Tyr Ala Arg Asn Gln Asn Ile Pro Phe Leu Thr Pro Pro Phe
 20 25 30
 Val Ser Ser Asp Gly Phe Gln Asn Phe Pro Pro Gly Val Leu Ser Leu
 35 40 45
 Lys Leu Ala Asp Pro Ile Ala Ile Val Asn Gly Asn Val Ser Leu Lys
 50 55 60
 Val Gly Gly Leu Thr Leu Gln Asp Gly Thr Gly Lys Leu Thr Val

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65	70	75	80
Asn Ala Asp Pro Pro Gln Leu Thr Asn Asn Lys Leu Gly Ile Ala			
85	90	95	
Leu Asp Ala Pro Phe Asp Val Ile Asp Asn Lys Leu Thr Leu Leu Ala			
100	105	110	
Gly His Gly Leu Ser Ile Ile Thr Lys Glu Thr Ser Thr Leu Pro Gly			
115	120	125	
Leu Arg Asn Thr Leu Val Val Leu Thr Gly Lys Gly Ile Gly Thr Glu			
130	135	140	
Ser Thr Asp Asn Gly Gly Thr Val Cys Val Arg Val Gly Glu Gly			
145	150	155	160
Gly Leu Ser Phe Asn Asn Asp Gly Asp Leu Val Ala Phe Asn Lys Lys			
165	170	175	
Glu Asp Lys Arg Thr Leu Trp Thr Thr Pro Asp Thr Ser Pro Asn Cys			
180	185	190	
Lys Ile Asp Gln Asp Lys Asp Ser Lys Leu Thr Leu Val Leu Thr Lys			
195	200	205	
Cys Gly Ser Gln Ile Leu Ala Asn Val Ser Leu Ile Val Val Asp Gly			
210	215	220	
Lys Tyr Lys Ile Ile Asn Asn Asn Thr Gln Pro Ala Leu Lys Gly Phe			
225	230	235	240
Thr Ile Lys Leu Leu Phe Asp Glu Asn Gly Val Leu Met Glu Ser Ser			
245	250	255	
Asn Leu Gly Lys Ser Tyr Trp Asn Phe Arg Asn Glu Asn Ser Ile Met			
260	265	270	
Ser Thr Ala Tyr Glu Lys Ala Ile Gly Phe Met Pro Asn Leu Val Ala			
275	280	285	
Tyr Pro Lys Pro Thr Ala Gly Ser Lys Lys Tyr Ala Arg Asp Ile Val			
290	295	300	
Tyr Gly Asn Ile Tyr Leu Gly Gly Lys Pro Asp Gln Pro Val Thr Ile			
305	310	315	320
Lys Thr Thr Phe Asn Gln Glu Thr Gly Cys Glu Tyr Ser Ile Thr Phe			
325	330	335	
Asp Phe Ser Trp Ala Lys Thr Tyr Val Asn Val Glu Phe Glu Thr Thr			
340	345	350	
Ser Phe Thr Phe Ser Tyr Ile Ala Gln Glu			
355	360		

<210> 42

<211> 20

<212> PRT

<213> Artificial Sequence

<220>

<223> Ad2 third repeat

<400> 42

Gly Asn Leu Thr Ser Gln Asn Val Thr Thr Val Thr Gln Pro Leu Lys

1

5

10

15

Lys Thr Lys Ser

20

<210> 43

<211> 20

<212> PRT

<213> Artificial Sequence

<220>

<223> Ad5 third repeat

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<400> 43
Gly Asn Leu Thr Ser Gln Asn Val Thr Thr Val Ser Pro Pro Leu Lys
1 5 10 15
Lys Thr Lys Ser
20

<210> 44
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Repeat motif

<221> VARIANT
<222> 4
<223> Xaa = Thr or Ser

<400> 44
Thr Thr Val Xaa
1

<210> 45
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Repeat Consensus Sequence

<221> VARIANT
<222> 3,5,7,13
<223> Xaa = Hydrophobic Amino Acid

<221> VARIANT
<222> 1, 2, 4, 6, 8, 9, 11, 12, 14, 15
<223> Xaa = Any Amino Acid

<221> VARIANT
<222> 10
<223> Xaa = Pro or Gly

<400> 45
Xaa
1 5 10 15

<210> 46
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Ad2 21st repeat

<400> 46
Gly Ala Met Ile Thr Lys Leu Gly Ala Gly Leu Ser Phe Asp Asn Ser
1 5 10 15

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<210> 47
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Ad5 21st repeat

<400> 47
Lys Ala Met Val Pro Lys Leu Gly Thr Gly Leu Ser Phe Asp Ser Thr
1 5 10 15

<210> 48
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Ad37 last repeat

<400> 48
Ile Gly Ile Asn Val Arg Ala Arg Glu Gly Leu Thr Phe Asp Asn Asp
1 5 10 15

<210> 49
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Last repeat consensus sequence

<221> VARIANT
<222> 4,7
<223> Xaa = Any Amino Acid

<221> VARIANT
<222> 9
<223> Xaa = Asp or Asn

<400> 49
Lys Leu Gly Xaa Gly Leu Xaa Phe Xaa
1 5

<210> 50
<211> 1164
<212> DNA
<213> Artificial Sequence

<220>
<223> Ad5D₈ fiber

<221> CDS
<222> (13) ... (1092)

<221> misc_feature
<222> 1130, 1157
<223> n = A, T, C or G

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<400> 50
atgggatcca ag atg aag cgc gca aga ccg tct gaa gat acc ttc aac ccc 51
Met Lys Arg Ala Arg Pro Ser Glu Asp Thr Phe Asn Pro
1 5 10

gtg tat cca tat gac acg gaa acc ggt cct cca act gtg cct ttt ctt 99
Val Tyr Pro Tyr Asp Thr Glu Thr Gly Pro Pro Thr Val Pro Phe Leu
15 20 25

act cct ccc ttt gta tcc ccc aat ggg ttt caa gag agt ccc cct ggg 147
Thr Pro Pro Phe Val Ser Pro Asn Gly Phe Gln Glu Ser Pro Pro Gly
30 35 40 45

gta ctc tct ttg cgc cta tcc gaa cct cta gtt acc tcc aat ggc atg 195
Val Leu Ser Leu Arg Leu Ser Glu Pro Leu Val Thr Ser Asn Gly Met
50 55 60

ctt gcg ctc aaa atg ggc aac ggc ctc tct ctg gac gag gcc ggc aac 243
Leu Ala Leu Lys Met Gly Asn Gly Leu Ser Leu Asp Glu Ala Gly Asn
65 70 75

ctt acc tcc caa aat gta acc act gtg agc cca cct ctc aaa aaa acc 291
Leu Thr Ser Gln Asn Val Thr Thr Val Ser Pro Pro Leu Lys Lys Thr
80 85 90

aag aaa aag ctt gaa gtt aac cta agc act gcc aag ggg ttg atg ttt 339
Lys Lys Lys Leu Glu Val Asn Leu Ser Thr Ala Lys Gly Leu Met Phe
95 100 105

gac gct aca gcc ata gcc att aat gca gga gat ggg ctt gaa ttt ggt 387
Asp Ala Thr Ala Ile Ala Ile Asn Ala Gly Asp Gly Leu Glu Phe Gly
110 115 120 125

tca cct aat gca cca aac aca aat ccc ctc aaa aca aaa att ggc cat 435
Ser Pro Asn Ala Pro Asn Thr Asn Pro Leu Lys Thr Lys Ile Gly His
130 135 140

ggc cta gaa ttt gat tca aac aag gct atg gtt cct aaa cta gga act 483
Gly Leu Glu Phe Asp Ser Asn Lys Ala Met Val Pro Lys Leu Gly Thr
145 150 155

ggc ctt agt ttt gac agc aca ggt gcc att aca gta gga aac aaa aat 531
Gly Leu Ser Phe Asp Ser Thr Gly Ala Ile Thr Val Gly Asn Lys Asn
160 165 170

aat gat aag cta act ttg tgg acc aca cca gct cca tct cct aac tgt 579
Asn Asp Lys Leu Thr Leu Trp Thr Thr Pro Ala Pro Ser Pro Asn Cys
175 180 185

aga cta aat gca gag aaa gat gct aaa ctc act ttg gtc tta aca aaa 627
Arg Leu Asn Ala Glu Lys Asp Ala Lys Leu Thr Leu Val Leu Thr Lys
190 195 200 205

tgt ggc agt caa ata ctt gct aca gtt tca gtt ttg gct gtt aaa ggc 675
Cys Gly Ser Gln Ile Leu Ala Thr Val Ser Val Leu Ala Val Lys Gly
210 215 220

agt ttg gct cca ata tct gga aca gtt caa agt gct cat ctt att ata 723
Ser Leu Ala Pro Ile Ser Gly Thr Val Gln Ser Ala His Leu Ile Ile
225 230 235

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aga ttt gac gaa aat gga gtg cta cta aac aat tcc ttc ctg gac cca	771
Arg Phe Asp Glu Asn Gly Val Leu Leu Asn Asn Ser Phe Leu Asp Pro	
240 245 250	
gaa tat tgg aac ttt aga aat gga gat ctt act gaa ggc aca gcc tat	819
Glu Tyr Trp Asn Phe Arg Asn Gly Asp Leu Thr Glu Gly Thr Ala Tyr	
255 260 265	
aca aac gct gtt gga ttt atg cct aac cta tca gct tat cca aaa tct	867
Thr Asn Ala Val Gly Phe Met Pro Asn Leu Ser Ala Tyr Pro Lys Ser	
270 275 280 285	
cac ggt aaa act gcc aaa agt aac att gtc agt caa gtt tac tta aac	915
His Gly Lys Thr Ala Lys Ser Asn Ile Val Ser Gln Val Tyr Leu Asn	
290 295 300	
gga gac aaa act aaa cct gta aca cta acc att aca cta aac ggt aca	963
Gly Asp Lys Thr Lys Pro Val Thr Leu Thr Ile Thr Leu Asn Gly Thr	
305 310 315	
cag gaa aca gga gac aca act cca agt gca tac tct atg tca ttt tca	1011
Gln Glu Thr Gly Asp Thr Thr Pro Ser Ala Tyr Ser Met Ser Phe Ser	
320 325 330	
tgg gac tgg tct ggc cac aac tac att aat gaa ata ttt gcc aca tcc	1059
Trp Asp Trp Ser Gly His Asn Tyr Ile Asn Glu Ile Phe Ala Thr Ser	
335 340 345	
tct tac act ttt tca tac att gcc caa gaa taa agaagcggcc gcgttatgaa	1112
Ser Tyr Thr Phe Ser Tyr Ile Ala Gln Glu *	
350 355	
gggcgaattc cagcacantg gcggccgtta ttagtggatc cgagntcatg ca	1164
<210> 51	
<211> 359	
<212> PRT	
<213> Artificial Sequence	
<220>	
<223> Ad5deltas	
<400> 51	
Met Lys Arg Ala Arg Pro Ser Glu Asp Thr Phe Asn Pro Val Tyr Pro	
1 5 10 15	
Tyr Asp Thr Glu Thr Gly Pro Pro Thr Val Pro Phe Leu Thr Pro Pro	
20 25 30	
Phe Val Ser Pro Asn Gly Phe Gln Glu Ser Pro Pro Gly Val Leu Ser	
35 40 45	
Leu Arg Leu Ser Glu Pro Leu Val Thr Ser Asn Gly Met Leu Ala Leu	
50 55 60	
Lys Met Gly Asn Gly Leu Ser Leu Asp Glu Ala Gly Asn Leu Thr Ser	
65 70 75 80	
Gln Asn Val Thr Thr Val Ser Pro Pro Leu Lys Lys Thr Lys Lys Lys	
85 90 95	
Leu Glu Val Asn Leu Ser Thr Ala Lys Gly Leu Met Phe Asp Ala Thr	
100 105 110	
Ala Ile Ala Ile Asn Ala Gly Asp Gly Leu Glu Phe Gly Ser Pro Asn	
115 120 125	
Ala Pro Asn Thr Asn Pro Leu Lys Thr Lys Ile Gly His Gly Leu Glu	
130 135 140	

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Phe Asp Ser Asn Lys Ala Met Val Pro Lys Leu Gly Thr Gly Leu Ser
 145 150 155 160
 Phe Asp Ser Thr Gly Ala Ile Thr Val Gly Asn Lys Asn Asn Asp Lys
 165 170 175
 Leu Thr Leu Trp Thr Thr Pro Ala Pro Ser Pro Asn Cys Arg Leu Asn
 180 185 190
 Ala Glu Lys Asp Ala Lys Leu Thr Leu Val Leu Thr Lys Cys Gly Ser
 195 200 205
 Gln Ile Leu Ala Thr Val Ser Val Leu Ala Val Lys Gly Ser Leu Ala
 210 215 220
 Pro Ile Ser Gly Thr Val Gln Ser Ala His Leu Ile Ile Arg Phe Asp
 225 230 235 240
 Glu Asn Gly Val Leu Leu Asn Asn Ser Phe Leu Asp Pro Glu Tyr Trp
 245 250 255
 Asn Phe Arg Asn Gly Asp Leu Thr Glu Gly Thr Ala Tyr Thr Asn Ala
 260 265 270
 Val Gly Phe Met Pro Asn Leu Ser Ala Tyr Pro Lys Ser His Gly Lys
 275 280 285
 Thr Ala Lys Ser Asn Ile Val Ser Gln Val Tyr Leu Asn Gly Asp Lys
 290 295 300
 Thr Lys Pro Val Thr Leu Thr Ile Thr Leu Asn Gly Thr Gln Glu Thr
 305 310 315 320
 Gly Asp Thr Thr Pro Ser Ala Tyr Ser Met Ser Phe Ser Trp Asp Trp
 325 330 335
 Ser Gly His Asn Tyr Ile Asn Glu Ile Phe Ala Thr Ser Ser Tyr Thr
 340 345 350
 Phe Ser Tyr Ile Ala Gln Glu
 355

<210> 52
 <211> 1920
 <212> DNA

<213> Artificial Sequence

<220>

<223> Ad5s/Ad37k fiber

<221> CDS

<222> (13) ... (1755)

<221> misc_feature

<222> 1867, 1875

<223> n = A,T,C or G

<400> 52

gcaagatcca ag atg aag cgc gca aga ccg tct gaa gat acc ttc aac ccc 51
 Met Lys Arg Ala Arg Pro Ser Glu Asp Thr Phe Asn Pro
 1 5 10

gtg tat cca tat gac acg gaa acc ggt cct cca act gtg cct ttt ctt 99
 Val Tyr Pro Tyr Asp Thr Glu Thr Gly Pro Pro Thr Val Pro Phe Leu
 15 20 25

act cct ccc ttt gta tcc ccc aat ggg ttt caa gag agt ccc cct ggg 147
 Thr Pro Pro Phe Val Ser Pro Asn Gly Phe Gln Glu Ser Pro Pro Gly
 30 35 40 45

gta ctc tct ttg cgc cta tcc gaa cct cta gtt acc tcc aat ggc atg 195
 Val Leu Ser Leu Arg Leu Ser Glu Pro Leu Val Thr Ser Asn Gly Met
 50 55 60

ctt	gct	ctc	aaa	atg	ggc	aac	ggc	ctc	tct	ctg	gac	gag	gcc	ggc	aac	243	
Leu	Ala	Leu	Lys	Met	Gly	Asn	Gly	Leu	Ser	Leu	Asp	Glu	Ala	Gly	Asn		
65								70				75					
ctt	acc	tcc	caa	aat	gta	acc	act	gtg	agc	cca	cct	ctc	aaa	aaa	acc	291	
Leu	Thr	Ser	Gln	Asn	Val	Thr	Thr	Val	Ser	Pro	Pro	Leu	Lys	Lys	Thr		
60								85				90					
aag	tca	aac	ata	aac	ctg	gaa	ata	tct	gca	ccc	ctc	aca	gtt	acc	tca	339	
Lys	Ser	Asn	Ile	Asn	Leu	Glu	Ile	Ser	Ala	Pro	Leu	Thr	Val	Thr	Ser		
95								100				105					
gaa	gcc	cta	act	gtg	gct	gcc	gca	cct	cta	atg	gtc	gct	ggc	aac	387		
Glu	Ala	Leu	Thr	Val	Ala	Ala	Ala	Ala	Pro	Leu	Met	Val	Ala	Gly	Asn		
110								115			120			125			
aca	ctc	acc	atg	caa	tca	cag	gcc	ccg	cta	acc	gtg	cac	gac	tcc	aaa	435	
Thr	Leu	Thr	Met	Gln	Ser	Gln	Ala	Pro	Leu	Thr	Val	His	Asp	Ser	Lys		
130								135				140					
ctt	agc	att	gcc	acc	caa	gga	ccc	cct	aca	gtg	tca	gaa	gga	aag	cta	483	
Leu	Ser	Ile	Ala	Thr	Gln	Gly	Pro	Leu	Thr	Val	Ser	Glu	Gly	Lys	Leu		
145								150				155					
gcc	ctg	caa	aca	tca	ggc	ccc	ctc	acc	acc	acc	acc	gat	agc	agt	acc	531	
Ala	Leu	Gln	Thr	Ser	Gly	Pro	Leu	Thr	Thr	Thr	Asp	Ser	Ser	Ser	Thr	Leu	
160								165				170					
act	atc	act	gcc	tca	ccc	cct	cta	act	act	gcc	act	ggt	agc	ttg	ggc	579	
Thr	Ile	Thr	Ala	Ser	Pro	Pro	Leu	Thr	Thr	Ala	Thr	Gly	Ser	Leu	Gly		
175								180				185					
att	gac	ttg	aaa	gag	ccc	att	tat	aca	caa	aat	gga	aaa	cta	gga	cta	627	
Ile	Asp	Leu	Lys	Glu	Pro	Ile	Tyr	Thr	Gln	Asn	Gly	Lys	Leu	Gly	Leu		
190								195			200			205			
aag	taa	ggg	gct	cct	ttg	cat	gta	aca	gac	gac	cta	aac	act	ttg	acc	675	
Lys	Tyr	Gly	Ala	Pro	Leu	His	Val	Thr	Asp	Asp	Leu	Asn	Thr	Leu	Thr		
210								215				220					
gta	gca	act	ggg	gtt	cca	ggg	gtt	act	att	aat	aat	act	tcc	ttg	caa	act	723
Val	Ala	Thr	Gly	Pro	Gly	Val	Thr	Ile	Asn	Asn	Thr	Ser	Leu	Gln	Thr		
225								230				235					
aaa	gtt	act	gga	gcc	ttg	ggg	ttt	gat	tca	caa	ggc	aat	atg	caa	ctt	771	
Lys	Val	Thr	Gly	Ala	Leu	Gly	Phe	Asp	Ser	Gln	Gly	Asn	Met	Gln	Leu		
240								245				250					
aat	gta	gca	gga	gga	cta	agg	att	gat	tct	caa	aac	aga	cgc	ctt	ata	819	
Asn	Val	Ala	Gly	Gly	Leu	Arg	Ile	Asp	Ser	Gln	Asn	Arg	Arg	Leu	Ile		
255								260				265					
ctt	gat	gtt	agt	tat	ccg	ttt	gat	gct	caa	aac	caa	cta	aat	cta	aga	867	
Leu	Asp	Val	Ser	Tyr	Pro	Phe	Asp	Ala	Gln	Gln	Leu	Asn	Leu	Arg			
270								275			280			285			
cta	gga	cag	ggc	cct	ctt	ttt	ata	aac	tca	gcc	cac	aac	ttg	gat	att	915	
Leu	Gly	Gln	Gly	Pro	Leu	Phe	Ile	Asn	Ser	Ala	His	Asn	Leu	Asp	Ile		
290								295				300					

aac tac aac aaa ggc ctt tac ttg ttt aca gct tca aac aat tcc aaa Asn Tyr Asn Lys Gly Leu Tyr Leu Phe Thr Ala Ser Asn Asn Ser Lys 305 310 315	963
aag ctt gag gtt aac cta agc act gcc aag ggg ttg atg ttt gac gct Lys Leu Glu Val Asn Leu Ser Thr Ala Lys Gly Leu Met Phe Asp Ala 320 325 330	1011
aca gcc ata gcc att aat gca gga gat ggg ctt gaa ttt ggt tca cct Thr Ala Ile Ala Ile Asn Ala Gly Asp Gly Leu Glu Phe Gly Ser Pro 335 340 345	1059
aat gca cca aac aca aat ccc ctc aaa aca aaa att ggc cat ggc cta Asn Ala Pro Asn Thr Asn Pro Leu Lys Thr Lys Ile Gly His Gly Leu 350 355 360 365	1107
gaa ttt gat tca aac aag gct atg gtt cct aaa cta gga act ggc ctt Glu Phe Asp Ser Asn Lys Ala Met Val Pro Lys Leu Gly Thr Gly Leu 370 375 380	1155
agt ttt gac agc aca ggt gcc att aca gta gga aac aaa aat aat gat Ser Phe Asp Ser Thr Gly Ala Ile Thr Val Gly Asn Lys Asn Asn Asp 385 390 395	1203
aag cta act ttg tgg acc aca cca gac act agt cca aac tgc aca att Lys Leu Thr Leu Trp Thr Pro Asp Thr Ser Pro Asn Cys Thr Ile 400 405 410	1251
gct caa gat aag gac tct aaa ctc act ttg gta ctt aca aag tgt gga Ala Gln Asp Lys Asp Ser Lys Leu Thr Leu Val Leu Thr Lys Cys Gly 415 420 425	1299
agt caa ata tta gct aat gtg tct ttg att gtg gtc gca gga aag tac Ser Gln Ile Leu Ala Asn Val Ser Leu Ile Val Val Ala Gly Lys Tyr 430 435 440 445	1347
cac atc ata aat aat aag aca aat cca aaa ata aaa agt ttt act att His Ile Ile Asn Asn Lys Thr Asn Pro Lys Ile Lys Ser Phe Thr Ile 450 455 460	1395
aaa ctg cta ttt aat aag aac gga gtg ctt tta gac aac tca aat ctt Lys Leu Leu Phe Asn Lys Asn Gly Val Leu Leu Asp Asn Ser Asn Leu 465 470 475	1443
gga aaa gct tat tgg aac ttt aga agt gga aat tcc aat gtt tcg aca Gly Lys Ala Tyr Trp Asn Phe Arg Ser Gly Asn Ser Asn Val Ser Thr 480 485 490	1491
gct tat gaa aaa gca att ggt ttt atg cct aat ttg gta gcg tat cca Ala Tyr Glu Lys Ala Ile Gly Phe Met Pro Asn Leu Val Ala Tyr Pro 495 500 505	1539
aaa ccc agt aat tct aaa aaa tat gca aga gac ata gtt tat gga act Lys Pro Ser Asn Ser Lys Lys Tyr Ala Arg Asp Ile Val Tyr Gly Thr 510 515 520 525	1587
ata tat ctt ggt gga aaa cct gat cag cca gca gtc att aaa act acc Ile Tyr Leu Gly Gly Lys Pro Asp Gln Pro Ala Val Ile Lys Thr Thr 530 535 540	1635
ttt aac caa gaa act gga tgt gaa tac tct atc aca ttt aac ttt agt	1683

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Phe Asn Gln Glu Thr Gly Cys Glu Tyr Ser Ile Thr Phe Asn Phe Ser
 545 550 555
 tgg tcc aaa acc tat gaa aat gtt gaa ttt gaa acc acc tct ttt acc 1731
 Trp Ser Lys Thr Tyr Glu Asn Val Glu Phe Glu Thr Thr Ser Phe Thr
 560 565 570
 ttc tcc tat att gcc caa gaa tga aaaagcggcc gctcgagtct agagggcccg 1785
 Phe Ser Tyr Ile Ala Gln Glu *
 575 580
 tttaaacccg ctgatcagcc tcgactgtgc cttctagttg ccagccatct gttgttgcc 1845
 cctcccccgt gccttccttg ancctggaa gtgcactcc cactgtcctt tcctaataaa 1905
 atgaggaat gcata 1920
 <210> 53
 <211> 580
 <212> PRT
 <213> Artificial Sequence
 <220>
 <223> Ad5s/Ad37k
 <400> 53
 Met Lys Arg Ala Arg Pro Ser Glu Asp Thr Phe Asn Pro Val Tyr Pro
 1 5 10 15
 Tyr Asp Thr Glu Thr Gly Pro Pro Thr Val Pro Phe Leu Thr Pro Pro
 20 25 30
 Phe Val Ser Pro Asn Gly Phe Gln Glu Ser Pro Pro Gly Val Leu Ser
 35 40 45
 Leu Arg Leu Ser Glu Pro Leu Val Thr Ser Asn Gly Met Leu Ala Leu
 50 55 60
 Lys Met Gly Asn Gly Leu Ser Leu Asp Glu Ala Gly Asn Leu Thr Ser
 65 70 75 80
 Gln Asn Val Thr Thr Val Ser Pro Pro Leu Lys Lys Thr Lys Ser Asn
 85 90 95
 Ile Asn Leu Glu Ile Ser Ala Pro Leu Thr Val Thr Ser Glu Ala Leu
 100 105 110
 Thr Val Ala Ala Ala Ala Pro Leu Met Val Ala Gly Asn Thr Leu Thr
 115 120 125
 Met Gln Ser Gln Ala Pro Leu Thr Val His Asp Ser Lys Leu Ser Ile
 130 135 140
 Ala Thr Gln Gly Pro Leu Thr Val Ser Glu Gly Lys Leu Ala Leu Gln
 145 150 155 160
 Thr Ser Gly Pro Leu Thr Thr Asp Ser Ser Thr Leu Thr Ile Thr
 165 170 175
 Ala Ser Pro Pro Leu Thr Thr Ala Thr Gly Ser Leu Gly Ile Asp Leu
 180 185 190
 Lys Glu Pro Ile Tyr Thr Gln Asn Gly Lys Leu Gly Leu Lys Tyr Gly
 195 200 205
 Ala Pro Leu His Val Thr Asp Asp Leu Asn Thr Leu Thr Val Ala Thr
 210 215 220
 Gly Pro Gly Val Thr Ile Asn Asn Thr Ser Leu Gln Thr Lys Val Thr
 225 230 235 240
 Gly Ala Leu Gly Phe Asp Ser Gln Gly Asn Met Gln Leu Asn Val Ala
 245 250 255
 Gly Gly Leu Arg Ile Asp Ser Gln Asn Arg Arg Leu Ile Leu Asp Val
 260 265 270
 Ser Tyr Pro Phe Asp Ala Gln Asn Leu Asn Leu Arg Leu Gly Gln
 275 280 285
 Gly Pro Leu Phe Ile Asn Ser Ala His Asn Leu Asp Ile Asn Tyr Asn

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290	295	300
Lys Gly Leu Tyr Leu Phe Thr Ala Ser Asn Asn Ser Lys Lys Leu Glu		
305	310	315
Val Asn Leu Ser Thr Ala Lys Gly Leu Met Phe Asp Ala Thr Ala Ile		320
325	330	335
Ala Ile Asn Ala Gly Asp Gly Leu Glu Phe Gly Ser Pro Asn Ala Pro		
340	345	350
Asn Thr Asn Pro Leu Lys Thr Lys Ile Gly His Gly Leu Glu Phe Asp		
355	360	365
Ser Asn Lys Ala Met Val Pro Lys Leu Gly Thr Gly Leu Ser Phe Asp		
370	375	380
Ser Thr Gly Ala Ile Thr Val Gly Asn Lys Asn Asn Asp Lys Leu Thr		
385	390	395
Leu Trp Thr Thr Pro Asp Thr Ser Pro Asn Cys Thr Ile Ala Gln Asp		400
405	410	415
Lys Asp Ser Lys Leu Thr Leu Val Leu Thr Lys Cys Gly Ser Gln Ile		
420	425	430
Leu Ala Asn Val Ser Leu Ile Val Val Ala Gly Lys Tyr His Ile Ile		
435	440	445
Asn Asn Lys Thr Asn Pro Lys Ile Lys Ser Phe Thr Ile Lys Leu Leu		
450	455	460
Phe Asn Lys Asn Gly Val Leu Leu Asp Asn Ser Asn Leu Gly Lys Ala		
465	470	475
Tyr Trp Asn Phe Arg Ser Gly Asn Ser Asn Val Ser Thr Ala Tyr Glu		
485	490	495
Lys Ala Ile Gly Phe Met Pro Asn Leu Val Ala Tyr Pro Lys Pro Ser		
500	505	510
Asn Ser Lys Lys Tyr Ala Arg Asp Ile Val Tyr Gly Thr Ile Tyr Leu		
515	520	525
Gly Gly Lys Pro Asp Gln Pro Ala Val Ile Lys Thr Thr Phe Asn Gln		
530	535	540
Glu Thr Gly Cys Glu Tyr Ser Ile Thr Phe Asn Phe Ser Trp Ser Lys		
545	550	555
Thr Tyr Glu Asn Val Glu Phe Glu Thr Thr Ser Phe Thr Phe Ser Tyr		560
565	570	575
Ile Ala Gln Glu		
580		

<210> 54
 <211> 1767
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Ad5s/Ad37s fiber

<221> CDS
 <222> (13) ... (1749)

<400> 54
 atgggatcca ag atg aag cgc gca aga ccg tct gaa gat acc ttc aac ccc 51
 Met Lys Arg Ala Arg Pro Ser Glu Asp Thr Phe Asn Pro
 1 5 10

gtg tat cca tat gac acg gaa acc ggt cct cca act gtg cct ttt ctt 99
 Val Tyr Pro Tyr Asp Thr Glu Thr Gly Pro Pro Thr Val Pro Phe Leu
 15 20 25

act cct ccc ttt gta tcc ccc aat ggg ttt caa gag agt ccc cct ggg 147
 Thr Pro Pro Phe Val Ser Pro Asn Gly Phe Gln Glu Ser Pro Pro Gly

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30	35	40	45	
gta ctc tct ttg cgc cta tcc gaa cct cta gtt acc tcc aat ggc atg Val Leu Ser Leu Arg Leu Ser Glu Pro Leu Val Thr Ser Asn Gly Met 50	55	60		195
ctt gcg ctc aaa atg ggc aac ggc ctc tct ctg gac gag gcc ggc agc Leu Ala Leu Lys Met Gly Asn Gly Leu Ser Leu Asp Glu Ala Gly Ser 65	70	75		243
cta act gta aac cct aag gct cca ctg caa gtt aat act gat tca aac Leu Thr Val Asn Pro Lys Ala Pro Leu Gln Val Asn Thr Asp Ser Asn 80	85	90		291
ata aac ctg gaa ata tct gca ccc ctc aca gtt acc tca gaa gcc cta Ile Asn Leu Glu Ile Ser Ala Pro Leu Thr Val Thr Ser Glu Ala Leu 95	100	105		339
act gtg gct gcc gca cct cta atg gtc gcg ggc aac aca ctc acc Thr Val Ala Ala Ala Pro Leu Met Val Ala Gly Asn Thr Leu Thr 110	115	120	125	387
atg caa tca cag gcc ccc cta acc gtg cac gac tcc aaa ctt agc att Met Gln Ser Gln Ala Pro Leu Thr Val His Asp Ser Lys Leu Ser Ile 130	135	140		435
gcc acc caa gga ccc ctc aca gtg tca gaa gga aag cta gcc ctg caa Ala Thr Gln Gly Pro Leu Thr Val Ser Glu Gly Lys Leu Ala Leu Gln 145	150	155		483
aca tca ggc ccc ctc acc acc acc gat agc agt acc ctt act atc act Thr Ser Gly Pro Leu Thr Thr Asp Ser Ser Thr Leu Thr Ile Thr 160	165	170		531
gcc tca ccc cct cta act act gcc act ggt agc ttg ggc att gac ttg Ala Ser Pro Pro Leu Thr Thr Ala Thr Gly Ser Leu Gly Ile Asp Leu 175	180	185		579
aaa gag ccc att tat aca caa aat gga aaa cta gga cta aag tac ggg Lys Glu Pro Ile Tyr Thr Gln Asn Gly Lys Leu Gly Leu Lys Tyr Gly 190	195	200	205	627
gct cct ttg cat gta aca gac gac cta aac act ttg acc gta gca act Ala Pro Leu His Val Thr Asp Asp Leu Asn Thr Leu Thr Val Ala Thr 210	215	220		675
ggt cca ggt gtg act att aat aat act tcc ttg caa act aaa gtt act Gly Pro Gly Val Thr Ile Asn Asn Thr Ser Leu Gln Thr Lys Val Thr 225	230	235		723
gga gcc ttg ggt ttt gat tca caa ggc aat atg caa ctt aat gta gca Gly Ala Leu Gly Phe Asp Ser Gln Gly Asn Met Gln Leu Asn Val Ala 240	245	250		771
gga gga cta agg att gat tct caa aac aga cgc ctt ata ctt gat gtt Gly Gly Leu Arg Ile Asp Ser Gln Asn Arg Arg Leu Ile Leu Asp Val 255	260	265		819
agt tat ccg ttt gat gct caa aac caa cta aat cta aga cta gga cag Ser Tyr Pro Phe Asp Ala Gln Asn Gln Leu Asn Leu Arg Leu Gly Gln 270	275	280	285	867

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ggc cct ctt ttt ata aac tca gcc cac aac ttg gat att aac tac aac	915
Gly Pro Leu Phe Ile Asn Ser Ala His Asn Leu Asp Ile Asn Tyr Asn	
290 295 300	
aaa ggc ctt tac ttg ttt aca gct tca aac aat tcc aaa aag ctt gag	963
Lys Gly Leu Tyr Leu Phe Thr Ala Ser Asn Asn Ser Lys Lys Leu Glu	
305 310 315	
gtt aac cta agc act gcc aag ggg ttg atg ttt gac gct aca gcc ata	1011
Val Asn Leu Ser Thr Ala Lys Gly Leu Met Phe Asp Ala Thr Ala Ile	
320 325 330	
gcc att aat gca gga gat ggg ctt gaa ttt ggt tca cct aat gca cca	1059
Ala Ile Asn Ala Gly Asp Gly Leu Glu Phe Gly Ser Pro Asn Ala Pro	
335 340 345	
aac aca aat ccc ctc aaa aca aaa att ggc cat ggc cta gaa ttt gat	1107
Asn Thr Asn Pro Leu Lys Thr Lys Ile Gly His Gly Leu Glu Phe Asp	
350 355 360 365	
tca aac att ggt ata aat gta aga gca aga gaa ggg ttg aca ttt gac	1155
Ser Asn Ile Gly Ile Asn Val Arg Ala Arg Glu Gly Leu Thr Phe Asp	
370 375 380	
aat gat ggt gcc att aca gta gga aac aaa aat aat gat aag cta act	1203
Asn Asp Gly Ala Ile Thr Val Gly Asn Lys Asn Asn Asp Lys Leu Thr	
385 390 395	
ttg tgg acc aca cca gct cca tct cct aac tgt aga cta aat gca gag	1251
Leu Trp Thr Thr Pro Ala Pro Ser Pro Asn Cys Arg Leu Asn Ala Glu	
400 405 410	
aaa gat gct aaa ctc act ttg gtc tta aca aaa tgt ggc agt caa ata	1299
Lys Asp Ala Lys Leu Thr Leu Val Leu Thr Lys Cys Gly Ser Gln Ile	
415 420 425	
ctt gct aca gtt tca gtt ttg gct gtt aaa ggc agt ttg gct cca ata	1347
Leu Ala Thr Val Ser Val Leu Ala Val Lys Gly Ser Leu Ala Pro Ile	
430 435 440 445	
tct gga aca gtt caa agt gct cat ctt att ata aga ttt gac gaa aat	1395
Ser Gly Thr Val Gln Ser Ala His Leu Ile Ile Arg Phe Asp Glu Asn	
450 455 460	
gga gtg cta cta aac aat tcc ttc ctg gac cca gaa tat tgg aac ttt	1443
Gly Val Leu Leu Asn Asn Ser Phe Leu Asp Pro Glu Tyr Trp Asn Phe	
465 470 475	
aga aat gga gat ctt act gaa ggc aca gcc tat aca aac gct gtt gga	1491
Arg Asn Gly Asp Leu Thr Glu Gly Thr Ala Tyr Thr Asn Ala Val Gly	
480 485 490	
ttt atg cct aac cta tca gct tat cca aaa tct cac ggt aaa act gcc	1539
Phe Met Pro Asn Leu Ser Ala Tyr Pro Lys Ser His Gly Lys Thr Ala	
495 500 505	
aaa agt aac att gtc agt caa gtt tac tta aac gga gac aaa act aaa	1587
Lys Ser Asn Ile Val Ser Gln Val Tyr Leu Asn Gly Asp Lys Thr Lys	
510 515 520 525	

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cct gta aca cta acc att aca cta aac ggt aca cag gaa aca gga gac	1635
Pro Val Thr Leu Thr Ile Thr Leu Asn Gly Thr Gln Glu Thr Gly Asp	
530 535 540	
aca act cca agt gca tac tct atg tca ttt tca tgg gac tgg tct ggc	1683
Thr Thr Pro Ser Ala Tyr Ser Met Ser Phe Ser Trp Asp Trp Ser Gly	
545 550 555	
cac aac tac att aat gaa ata ttt gcc aca tcc tct tac act ttt tca	1731
His Asn Tyr Ile Asn Glu Ile Phe Ala Thr Ser Ser Tyr Thr Phe Ser	
560 565 570	
tac att gcc caa gaa taa agaagcggcc gcgttatg	1767
Tyr Ile Ala Gln Glu *	
575	

<210> 55
<211> 578
<212> PRT
<213> Artificial Sequence

<220>
<223> Ad5s/Ad37s

<400> 55	
Met Lys Arg Ala Arg Pro Ser Glu Asp Thr Phe Asn Pro Val Tyr Pro	
1 5 10 15	
Tyr Asp Thr Glu Thr Gly Pro Pro Thr Val Pro Phe Leu Thr Pro Pro	
20 25 30	
Phe Val Ser Pro Asn Gly Phe Gln Glu Ser Pro Pro Gly Val Leu Ser	
35 40 45	
Leu Arg Leu Ser Glu Pro Leu Val Thr Ser Asn Gly Met Leu Ala Leu	
50 55 60	
Lys Met Gly Asn Gly Leu Ser Leu Asp Glu Ala Gly Ser Leu Thr Val	
65 70 75 80	
Asn Pro Lys Ala Pro Leu Gln Val Asn Thr Asp Ser Asn Ile Asn Leu	
85 90 95	
Glu Ile Ser Ala Pro Leu Thr Val Thr Ser Glu Ala Leu Thr Val Ala	
100 105 110	
Ala Ala Ala Pro Leu Met Val Ala Gly Asn Thr Leu Thr Met Gln Ser	
115 120 125	
Gln Ala Pro Leu Thr Val His Asp Ser Lys Leu Ser Ile Ala Thr Gln	
130 135 140	
Gly Pro Leu Thr Val Ser Glu Gly Lys Leu Ala Gln Thr Ser Gly	
145 150 155 160	
Pro Leu Thr Thr Asp Ser Ser Thr Leu Thr Ile Thr Ala Ser Pro	
165 170 175	
Pro Leu Thr Thr Ala Thr Gly Ser Leu Gly Ile Asp Leu Lys Glu Pro	
180 185 190	
Ile Tyr Thr Gln Asn Gly Lys Leu Gly Leu Lys Tyr Gly Ala Pro Leu	
195 200 205	
His Val Thr Asp Asp Leu Asn Thr Leu Thr Val Ala Thr Gly Pro Gly	
210 215 220	
Val Thr Ile Asn Asn Thr Ser Leu Gln Thr Lys Val Thr Gly Ala Leu	
225 230 235 240	
Gly Phe Asp Ser Gln Gly Asn Met Gln Leu Asn Val Ala Gly Gly Leu	
245 250 255	
Arg Ile Asp Ser Gln Asn Arg Arg Leu Ile Leu Asp Val Ser Tyr Pro	
260 265 270	
Phe Asp Ala Gln Asn Gln Leu Asn Leu Arg Leu Gly Gln Gly Pro Leu	

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275	280	285
Phe Ile Asn Ser Ala His Asn	Leu Asp Ile Asn	Tyr Asn Lys Gly Leu
290	295	300
Tyr Leu Phe Thr Ala Ser Asn Asn Ser Lys	Lys Leu Glu Val Asn	Leu
305	310	315
Ser Thr Ala Lys Gly Leu Met Phe Asp	Ala Thr Ala Ile Ala	Ile Asn
325	330	335
Ala Gly Asp Gly Leu Glu Phe Gly Ser Pro Asn	Ala Pro Asn Thr Asn	
340	345	350
Pro Leu Lys Thr Lys Ile Gly His	Gly Leu Glu Phe Asp Ser Asn	Ile
355	360	365
Gly Ile Asn Val Arg Ala Arg	Glu Gly Leu Thr Phe Asp Asn Asp	Gly
370	375	380
Ala Ile Thr Val Gly Asn Lys Asn Asn Asp	Lys Leu Thr Leu Trp	Trp Thr
385	390	395
Thr Pro Ala Pro Ser Pro Asn Cys Arg	Leu Asn Ala Glu Lys Asp	Ala
405	410	415
Lys Leu Thr Leu Val Leu Thr Lys Cys Gly Ser Gln	Ile Leu Ala Thr	
420	425	430
Val Ser Val Leu Ala Val Lys Gly Ser	Leu Ala Pro Ile Ser Gly	Thr
435	440	445
Val Gln Ser Ala His Leu Ile Ile Arg Phe Asp	Glu Asn Gly Val	Leu
450	455	460
Leu Asn Asn Ser Phe Leu Asp Pro Glu Tyr Trp	Asn Phe Arg Asn	Gly
465	470	475
Asp Leu Thr Glu Gly Thr Ala Tyr Thr Asn	Ala Val Gly Phe Met	Pro
485	490	495
Asn Leu Ser Ala Tyr Pro Lys Ser His Gly	Lys Thr Ala Lys Ser	Asn
500	505	510
Ile Val Ser Gln Val Tyr Leu Asn Gly Asp	Lys Thr Lys Pro Val	Thr
515	520	525
Leu Thr Ile Thr Leu Asn Gly Thr Gln Glu Thr	Gly Asp Thr Thr	Pro
530	535	540
Ser Ala Tyr Ser Met Ser Phe Ser Trp Asp	Trp Ser Gly His Asn	Tyr
545	550	555
Ile Asn Glu Ile Phe Ala Thr Ser Ser	Tyr Thr Phe Ser Tyr	Ile Ala
565	570	575
Gln Glu		

<210> 56
 <211> 1132
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Ad37s/Ad5k fiber

<221> CDS

<222> (16) ... (1116)

<221> misc_feature

<222> 1125

<223> n = A, T, C or G

<400> 56

gtcgcaagat ccaag atg aag agg gcc cgg ccc agc gaa gat gac ttc aac 51
 Met Lys Arg Ala Arg Pro Ser Glu Asp Asp Phe Asn
 1 5 10

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ccc gtc tac ccc tat ggc tac gcg cg ^g aat cag aat atc ccc ttc ctc	99
Pro Val Tyr Pro Tyr Gly Tyr Ala Arg Asn Gln Asn Ile Pro Phe Leu	
15 20 25	
act ccc ccc ttt gtc tcc tcc gat gga ttc aaa aac ttc ccc cct ggg	147
Thr Pro Pro Phe Val Ser Ser Asp Gly Phe Lys Asn Phe Pro Pro Gly	
30 35 40	
gta ctg tca ctc aaa ctg gct gat cca atc acc att acc aat ggg gat	195
Val Leu Ser Leu Lys Leu Ala Asp Pro Ile Thr Ile Thr Asn Gly Asp	
45 50 55 60	
gta tcc ctc aag gt ^g gga ggt ggt ctc act ttg caa gat gga agc cta	243
Val Ser Leu Lys Val Gly Gly Leu Thr Leu Gln Asp Gly Ser Leu	
65 70 75	
act gta aac cct aag gct cca ctg caa gtt aat act gat aaa aaa ctt	291
Thr Val Asn Pro Lys Ala Pro Leu Gln Val Asn Thr Asp Lys Lys Leu	
80 85 90	
gag ctt gca tat gat aat cca ttt gaa agt agt gct aat aaa ctt agt	339
Glu Leu Ala Tyr Asp Asn Pro Phe Glu Ser Ser Ala Asn Lys Leu Ser	
95 100 105	
tta aaa gta gga cat gga tta aaa gta tta gat gaa aaa agt gct gcg	387
Leu Lys Val Gly His Gly Leu Lys Val Leu Asp Glu Lys Ser Ala Ala	
110 115 120	
ggg tta aaa gat tta att ggc aaa ctt gt ^g gtt tta aca gga aaa gga	435
Gly Leu Lys Asp Leu Ile Gly Lys Leu Val Val Leu Thr Gly Lys Gly	
125 130 135 140	
ata ggc act gaa aat tta gaa aat aca gat ggt agc agc aga gga att	483
Ile Gly Thr Glu Asn Leu Glu Asn Thr Asp Gly Ser Ser Arg Gly Ile	
145 150 155	
ggt ata aat gta aga gca aga gaa ggg ttg aca ttt gac aat gat gga	531
Gly Ile Asn Val Arg Ala Arg Glu Gly Leu Thr Phe Asp Asn Asp Gly	
160 165 170	
tac ttg gta gca tgg aac cca aag tat gac acg cgc act ttg tgg acc	579
Tyr Leu Val Ala Trp Asn Pro Lys Tyr Asp Thr Arg Thr Leu Trp Thr	
175 180 185	
aca cca gct cca tct cct aac t ^g t aga cta aat gca gag aaa gat gct	627
Thr Pro Ala Pro Ser Pro Asn Cys Arg Leu Asn Ala Glu Lys Asp Ala	
190 195 200	
aaa ctc act ttg gtc tta aca aaa t ^g t ggc agt caa ata ctt gct aca	675
Lys Leu Thr Leu Val Leu Thr Lys Cys Gly Ser Gln Ile Leu Ala Thr	
205 210 215 220	
gtt tca gtt ttg gct gtt aaa ggc agt ttg gct cca ata tct gga aca	723
Val Ser Val Leu Ala Val Lys Gly Ser Leu Ala Pro Ile Ser Gly Thr	
225 230 235	
gtt caa agt gct cat ctt att ata aga ttt gac gaa aat gga gt ^g cta	771
Val Gln Ser Ala His Leu Ile Ile Arg Phe Asp Glu Asn Gly Val Leu	
240 245 250	
cta aac aat tcc ttc ctg gat cca gaa tat tgg aac ttt aga aat gga	819

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Leu Asn Asn Ser Phe Leu Asp Pro Glu Tyr Trp Asn Phe Arg Asn Gly
 255 260 265
 gat ctt act gaa ggc aca gcc tat aca aac gct gtt gga ttt atg cct 867
 Asp Leu Thr Glu Gly Thr Ala Tyr Thr Asn Ala Val Gly Phe Met Pro
 270 275 280
 sac cta tca gct tat cca aaa tct cac ggt aaa act gcc aaa agt aac 915
 Asn Leu Ser Ala Tyr Pro Lys Ser His Gly Lys Thr Ala Lys Ser Asn
 285 290 295 300
 att gtc agt caa gtt tac tta aac gga gac aaa act aaa cct gta aca 963
 Ile Val Ser Gln Val Tyr Leu Asn Gly Asp Lys Thr Lys Pro Val Thr
 305 310 315
 cta acc att aca aac ggt aca cag gaa aca gga gac aca act cca 1011
 Leu Thr Ile Thr Leu Asn Gly Thr Gln Glu Thr Gly Asp Thr Thr Pro
 320 325 330
 agt gca tac tct atg tca ttt tca tgg gac tgg tct ggc cac aac tac 1059
 Ser Ala Tyr Ser Met Ser Phe Ser Trp Asp Trp Ser Gly His Asn Tyr
 335 340 345
 att aat gaa ata ttt gcc aca tcc tct tac act ttt tca tac att gcc 1107
 Ile Asn Glu Ile Phe Ala Thr Ser Ser Tyr Thr Phe Ser Tyr Ile Ala
 350 355 360
 caa gaa taa agaagcggnc gctcga 1132
 Gln Glu *
 365

<210> 57
 <211> 366
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Ad37s/Ad5k

<400> 57
 Met Lys Arg Ala Arg Pro Ser Glu Asp Asp Phe Asn Pro Val Tyr Pro
 1 5 10 15
 Tyr Gly Tyr Ala Arg Asn Gln Asn Ile Pro Phe Leu Thr Pro Pro Phe
 20 25 30
 Val Ser Ser Asp Gly Phe Lys Asn Phe Pro Pro Gly Val Leu Ser Leu
 35 40 45
 Lys Leu Ala Asp Pro Ile Thr Ile Thr Asn Gly Asp Val Ser Leu Lys
 50 55 60
 Val Gly Gly Leu Thr Leu Gln Asp Gly Ser Leu Thr Val Asn Pro
 65 70 75 80
 Lys Ala Pro Leu Gln Val Asn Thr Asp Lys Lys Leu Glu Leu Ala Tyr
 85 90 95
 Asp Asn Pro Phe Glu Ser Ser Ala Asn Lys Leu Ser Leu Lys Val Gly
 100 105 110
 His Gly Leu Lys Val Leu Asp Glu Lys Ser Ala Ala Gly Leu Lys Asp
 115 120 125
 Leu Ile Gly Lys Leu Val Val Leu Thr Gly Lys Gly Ile Gly Thr Glu
 130 135 140
 Asn Leu Glu Asn Thr Asp Gly Ser Ser Arg Gly Ile Gly Ile Asn Val
 145 150 155 160

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Arg Ala Arg Glu Gly Leu Thr Phe Asp Asn Asp Gly Tyr Leu Val Ala
 165 170 175
 Trp Asn Pro Lys Tyr Asp Thr Arg Thr Leu Trp Thr Thr Pro Ala Pro
 180 185 190
 Ser Pro Asn Cys Arg Leu Asn Ala Glu Lys Asp Ala Lys Leu Thr Leu
 195 200 205
 Val Leu Thr Lys Cys Gly Ser Gln Ile Leu Ala Thr Val Ser Val Leu
 210 215 220
 Ala Val Lys Gly Ser Leu Ala Pro Ile Ser Gly Thr Val Gln Ser Ala
 225 230 235 240
 His Leu Ile Ile Arg Phe Asp Glu Asn Gly Val Leu Leu Asn Asn Ser
 245 250 255
 Phe Leu Asp Pro Glu Tyr Trp Asn Phe Arg Asn Gly Asp Leu Thr Glu
 260 265 270
 Gly Thr Ala Tyr Thr Asn Ala Val Gly Phe Met Pro Asn Leu Ser Ala
 275 280 285
 Tyr Pro Lys Ser His Gly Lys Thr Ala Lys Ser Asn Ile Val Ser Gln
 290 295 300
 Val Tyr Leu Asn Gly Asp Lys Thr Lys Pro Val Thr Leu Thr Ile Thr
 305 310 315 320
 Leu Asn Gly Thr Gln Glu Thr Gly Asp Thr Thr Pro Ser Ala Tyr Ser
 325 330 335
 Met Ser Phe Ser Trp Asp Trp Ser Gly His Asn Tyr Ile Asn Glu Ile
 340 345 350
 Phe Ala Thr Ser Ser Tyr Thr Phe Ser Tyr Ile Ala Gln Glu
 355 360 365

<210> 58

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Ad37 third repeat

<400> 58

Gly Ser Leu Thr Val Asn Pro Lys Ala Pro Leu Gln Val Asn Thr Asp
 1 5 10 15

<210> 59

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> Ad8 last repeat

<400> 59

Val Arg Val Gly Glu Gly Gly Gly Leu Ser Phe Asn Asp Asn
 1 5 10

<210> 60

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> Ad9 last repeat

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<400> 60
Val Arg Val Gly Glu Gly Gly Leu Ser Phe Asn Asn Asp .
1 5 10

<210> 61
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Ad15 last repeat

<400> 61
Val Arg Val Gly Glu Gly Gly Leu Ser Phe Asn Glu Ala
1 5 10

<210> 62
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Penton region

<400> 62
His Ala Ile Arg Gly Asp Thr Phe
1 5

<210> 63
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Penton amino acid replacement

<400> 63
Ser Arg Gly Tyr Pro Tyr Asp Val Pro Asp Tyr Ala Gly Thr Ser
1 5 10 15

<210> 64
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Fiber protein conserved sequence

<400> 64
Thr Trp Leu Thr
1

<210> 65
<211> 4
<212> PRT
<213> Artificial Sequence

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<220>
<223> HSP binding motif

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Lys Lys Thr Lys
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